Fri

protein search, using sw model • OM protein March 16, 2006, 15:49:10 ; Search time 188 Seconds (without alignments) 495.470 Million cell updates/sec Run on:

US-09-989-830-238

1134 1 SPHQAAAPVDQTPRTLATMG.....RRWAVAPCRAEKLMCSSSRS 212 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 seqs, 439378781 residues Searched:

2443163 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 8 08 08 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* A Geneseq 21:* 1: geneseqp198 Database

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITAMADIDO

		a			SUMMARIES	
Result No.	Score	Query Match	ð Query Match Length DB	DB	ID	Description
	1134	100.0	212	9	ABJ18429	Abil8429 Breast sp
8	1134	100.0	217	7	ADD01203	
3	1134	100.0	217	0	AEA20112	
4	1069.5	94.3	213	ß	ABU60984	Abu60984 Lung spec
S	1069.5	94.3	213	ഗ	ABU60939	Lung
9	1065.5	94.0	218	2	ABJ05501	Humar
7	154	13.6	559	æ	ADQ67157	Add67157 Novel hum
60	154	13.6	1127	4	AAB95541	Aab95541 Human pro
σ	154	13.6	1480	7	ADJ70433	Human
10	154	13.6	2427	œ	ADR09758	Adr09758 Human pro
11	154	13.6	2735	9	ABR41356	
12	154	13.6	2971	m	AAB41231	Aab41231 Human ORF
13	152	13.4	2971	7	ADC35084	Adc35084 Human bre
14	152	13.4	2972	4	AAB50363	Aab50363 Human SRC
15	152	13.4	3118	4	AAB50362	Aab50362 Human SRC
16	149.5	13.2	1828	4	ABB50164	Abb50164 Human tra
17	141	12.4	1008	4	ABB11527	Abb11527 Human apo
18	140.5	12.4	325	7	ABM87858	Rice a
19	138.5	12.2	532	٣	AAY84593	
20	138	12.2	346	-	ABM89803	Abm89803 Rice abio
21	136.5	12.0	415	4	ABG30150	Abg30150 Novel hum
22	135.5	11.9	693	ស	ABP69529	Abp69529 Human pol
23	135.5	11.9	842	4	ABB66631	Drosog
24	135.5	11.9	864	4	ABB71319	Abb71319 Drosophil

Adm05164 Human pro Ads15467 HSV-1 pol Abo69351 Beeudomon		Aam58086 Human bra Abg40187 Human pep Adx05726 Cyclin-de			Aae33867 Human RIZ Abu62110 Human ret Abu62116 Human RIZ
7 ADMO5164 8 ADS15467 7 ABO69351	4 ABB32160 4 ABB22702 4 AAM70534	4 AAM58086 5 ABG40187 9 ADX05726 6 AAR33868	ABUG2117 AAR92100 AAR92113 ABR12013	3 AAB12114 5 AAU10788 5 AAU80804	6 AAE33867 6 ABU62110 6 ABU62116
3164 308	0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	983 983 1482	1718	1719	1719 1719 1719
6.6.6.6	6.11.6	6.11.6		11.9	11.9
135	134.5	134.5 134.5 134.5	134.45 134.55 134.55 15.75 15.75	134.5 134.5	134.5 134.5 134.5
25 27 27	3000	8 8 8 8 8 8 4 8	, w w w w	4 4 4 0 1 4	4 4 4 6 4 7

ALIGNMENTS

Breast specific related amino acid sequence SEQ ID No 238 ABJ18429 standard; protein; 212 AA. (first entry) 30-JAN-2003 ABJ18429; RESULT 1 ABJ18429 ID ABJ1

Cytostatic; BSP-agonist; BSP-antagonist; vaccine; gene therapy; cancer; metastatic; breast cancer; breast specific; human.

Homo sapiens.

WO200277232-A2.

03-OCT-2002.

21-NOV-2001; 2001WO-US043815.

22-NOV-2000; 2000US-0252509P.

(DIAD-) DIADEXUS INC.

Liu C; Sun Y, Pluta J, Recipon H, Macina RA, Salceda S,

WPI; 2003-018927/01.

New isolated nucleic acid molecule, useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient.

Claim 11; Page 355; 377pp; English.

The invention relates to a novel isolated nucleic acid molecule comprising: a sequence encoding a sequence comprising 11-1518 amino acids ; a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides of the invention can be used to treat disorders by gene therapy. This sequence represents a breast specific related polypeptide of the invention

Sequence 212 AA;

Claim 1; SEQ ID NO 41; 405pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; hepatotropic; antibacterial; virucide; protozoacide; antiparastitic; fungicide; gene therapy; cell proliferative disease; cancer; atherosclerosis; hepatitis; neurological disorder; Parkinson's disease; Alzheimer's disease; stroke; epilepsy; developmental disorder; renal tubular acidosis; anaemia; glaucoma; hypothyroidism; autoimmune disorder; inflammatory disorder; AIDS; allergy;
                                                                                                                                         AGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQP
                                                            SPHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAA
                                                                                         SPHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAA
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                                Gaps
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Forsythe IJ, Gorrad AB, Griffin JA;
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 Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human nucleic acid-associated protein NAAP-41 SEQ ID NO:41.
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; nucleic acid-associated protein; NAAP; cytostatic;
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100.0%; Score 1134; DB 6;
100.0%; Pred. No. 3.9e-80;
ive 0; Mismatches 0;
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25-JAN-2002; 2002US-0351749P.
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                             212; Conservative
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N-PSDB; ADD01260.
 Query Match
Best Local Similarity
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The present invention describes human nucleic acid-associated proteins designated NAAP-1 to NAAP-57. The human NAAPs have cytostatic, antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective, antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective, antiarteriosclerotic, ophthalmological, thyromimetic, antiparasitic antiarteriotic antibacterial, virucide, protozoacide, antiparasitic and materiotide activities, and can be used in gene therapy. The NAAP protein and polynucleotide sequences can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased corpression or overagression of NAAP, such as cell proliferative diseases (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (evelopmental disorders (renal tubular acidosis, ansemia, glaucoma, hypothyroidism), autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis, arthritis) and infections (e.g. bacterial, viral, parasitic, protozoal, fungal). The present sequence represents human NAAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary; CNS-gen.; gene therapy; diagnostic; forensic; mapping; DNA purification; protein purification; osteoarthritis; antiarthritic; osteogathic; musculoskeletal disease; osteoporosis; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy; Aliahelmers disease; neuroprotective; nootropic; degeneration; parkinsons disease; antiparkinsonian; neurological disease; cerebrovascular ischemia; cerebroprotective; vasotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1134; DB 7; Length 100.0%; Pred. No. 4e-80; ive 0; Mismatches 0; Indels
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Matches 212; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 217 AA;
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Best Local A
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                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new isolated polymucleotide (I) encoding a polypeptide with biological activity comprising: a nucleotide sequence of $80 ID NOS: 1-567 (iluly defined); a mucleotide sequence that hybridizes to the sequence having greater than $9$ sequence identity with the sequence of (il). Also described are: a(n) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polymucleotide in the host cell; an isolated polypeptide comprising a sequence of $80 ID NOS: 568-1134 (fully defined), where the polypeptide (I); an a polypeptide encoded by a composition comprising the polypeptide of (3) and a carrier; an antibody directed against the polypeptide of (3) and a carrier; an antibody directed against the polypeptide of (3); a method for identifying a compound that binds to the collection of polymucleotides, where the collection comprising of at collection of polymucleotides, where the collection comprising of at collection of polymucleotides, where the collection comprising any of the sequences of $80 ID NOS: 1-567. (I) is a polymucleotide comprising any of the sequences of $80 ID NOS: 1-567. (I) is a polymucleotide comprising of activity, which comprises any of the amino acid sequence of $80 ID NOS: 1-567. (I) is a polymucleotide comprising of mutations responsible for genetic disorders or types of data and products dependent on DNA and amino acid sequences. The composition and method are useful in diagnostics, forensic, and gene mapping, in identifying of mutations responsible for genetic disorders or composition and method are useful for treating a disease or disorder. C sequence of a total polypeptide of the invention. This is the amino acid sequence of a novel polypeptide of the invention.
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                                                                                                                                                                                                                            New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral
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                                                                  Zhou P, Ma Y;
Goodrich R, Chen
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                                                                  Ren F,
Wang D,
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                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 806; 500pp; English.
                                                               Wang J, Wang ZW, Zhang J,
Xue A, Asundi V, Zhao Q,
Weng G, Boyle B;
                                                                                                                                                                                                                                                                                                        infection, or cancer.
                                                                                                                                                          WPI; 2005-417730/42
                   (NUVE-) NUVELO INC.
                                                                                                                                                                                     N-PSDB; AEA19545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 217 AA;
                                                                                                              Wehrman T,
                                                               Tang TY,
Ghosh M,
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121 PWAAASATPMLSSKASLCIPTERPPQPLMRTPAARSHWPIPHPASTACPAPLPVVLVAP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                    Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.3%; Score 1069.5; DE
95.3%; Pred. No. 4e-75;
ive 1; Mismatches
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ABU60984 standard; protein; 213 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-2001; 2001WO-US043612.
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                                                                                                                                                                               Lung specific protein (LSP)
                                                                                                                   (first entry)
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nes 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DIAD-) DIADEXUS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                      WO200268633-A2.
                                                                                                                   08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                           ABU60984;
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12-FEB-2002; 2002WO-US004197.
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              (first entry)
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                                                                                                                                                                                                                                                                                                                                                       Macina RA,
                                                                                                                                                                                                                                                                                                                  (DIAD-) DIADEXUS INC
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                                                                                                                                                                           WO200264611-A1
                                                                                                                                                                                                                                                                                                                                                     Salceda S, Ma
Sun Y. Liu C;
              14-NOV-2002
                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                         Sun Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMA-SGSSQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PWAAASATPMLSSKASLCIPTRGPPPOPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 140-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, invention are useful for identifying, diagnosing, monitoring staging, they are also used for identifying lung tissus, monitoring and identifying and/or designing antagonists of the polypeptide of the inng. Invention, gene therapy, production of transgenic animals and production of engineered lung tissus for treatment and research. This is the amino acid sequence of a lung specific nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SPHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                      Human; gene therapy, vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SPHOAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
94.3%; Score 1069.5; DE
Best Local Similarity 95.3%; Pred. No. 4e-75;
Matches 203; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Liu
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                                                                                                                                                                                                                                                                                                                                                                                                            Sun
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                                                                                      specific protein (LSP) #42
                                                                                                                                                                                                                                                                                                                                                                                                            Chen S,
                                                                                                                                                                                                                                                                                                   21-NOV-2001; 2001WO-US043612
                                                                                                                                                                                                                                                                                                                                      22-NOV-2000; 2000US-0252500P
                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                        (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-713376/77.
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                                                                                                                                                                                                                             WO200268633-A2
                                                                                                                                                                                            Homo sapiens
                                                 08-MAY-2003
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              ABU60939
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ABJ05501

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179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMA-SGSSQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer and non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is a polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWAAASATPMLSSKASLCIPTRGPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SPHOAAAPVDOTPRTLATMGORALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAA
                                        Human, breast specific gene, breast specific protein, breast cancer, gene therapy, cytostatic.
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  261.
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Pred. No. 8.3e-75;
1; Mismatches 8; Indels
Human breast cancer associated polypeptide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    Karra K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212
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                                                                                                                                                                                                                                                                                                                                                                                                                    Recipon H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 339-340; 367pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hu P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                  The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morphid setates. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 PAPASAPLTIPISAPLTVSASG----PALLTSVTPPLAPVVPAAPGPPSLAPSGASPSAS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 VLAPSPGAAPVLASSQTPVPVWAPSSTPGTSLASASPVPAPTPVLAPSSTOTMLPAPVPS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 KPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP---- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 ----PQPLMRTPAARSHWPIP--HPCDT-----ACPAPLPVVLVAPRST------ 182
                                                                                                                                                                                                                             Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PHOAAAPVD---QTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 A-AAGIA------SSAVEPVCGDA-APACLLRTPLRGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 NPAPAQASLIAP-----ASSASQALATPIA-PWAAPQTAILAPSPAPPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                           Ishii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    80;
                                                                                                                                                                                                                                                                                                                                                                                                                           13.6%; Score 154; DB 8; Length 559; 25.7%; Pred. No. 0.0013; ive 27; Mismatches 92; Indels 8
                                                                                                                                                           Sato H,
                                                                                                                                                          Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 PLPSPASTOTL---ALAPALAPTIGGSS 344
                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4318; 2449pp; English.
                                                                                                                                                  Otsuki T, Wax....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein sequence SEQ ID NO:18149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB95541 standard; protein; 1127 AA
                                                                                                                                                                      Nagai K,
                                                                                                                                    (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                             21-JAN-2004; 2004EP-00001196
                                                                                                 21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 25.74 es 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                    dementia and various cance sequence of the invention
                                                                                                                                                         Sugiyama T,
, Isono Y,
                                                                                                                                                                                            WPI; 2004-535376/52.
                                                                                                                                                                                                       N-PSDB; ADQ64969
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 559 AA;
           Homo sapiens
                                EP1440981-A2
                                                                                                                                                                      Yamamoto J,
                                                      28-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-2001
                                                                                                                                                          Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB95541;
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Matches
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The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonuclectide complementary to the
complementary strand of a polynuclectide which comprises one of the 5602

(c) complementary strand of a polynuclectide which comprises one of the 5602

(c) c) constant sets at least 15 nucleotides; or (b) a combination

(c) an oligonuclectide comprising a sequence complementary to the
complementary strand of a polynuclectide which comprises a 5'-end

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising a sequence complementary to a

(c) sequence and an oligonuclectide comprising polynuclectides,

(c) sequence and an oligonuclectide comprises are also useful for the

(c) particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers also useful for the full-leng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18472 represent human cDNA sequences; AAB22446 to AAB35893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               721 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   828 VLAPSPGAAAPVLASSQTPVPVMAPSSTPGTSLASASPVPAPTPVLAPSSTQTMLPAPVPS 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynuclectides, particularly the 5602 full length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |:||:
PAPASAPLTIPISAPLTVSASG----PALLTSVTPPLAPVVPAAPGPPSLAPSGASPSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K, Ye Otsuki T,
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Wakamatsu A, Nagai K,
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Sugiyama T, Wakamatsu
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09-JUN-2000; 2000JP-00241899
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11-JAN-2000;
Homo sapiens
                                                                                  EP1074617-A2
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                                                                                                                                                                                   07-FEB-2001
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERAP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart control of the invention.
                                                                                                                                                                                                                                                                                             Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                           Human heat mitochondrial protein as a therapeutic target SeqID2239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gibson BW, Taylor SW, Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.6%; Score 154; DB 7; Length 1480; 25.7%; Pred. No. 0.0035; 25.7%; Mismatches 92; Indels 80
                                                                                                                                                                                                                                                            assay; diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                  osteopathic; ophthalmological; cytostatic.
183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
                                888 PLPSPASTOTL -- ALAPALAPTIGGSS 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 2239; 180pp; English.
                                                                                                                                                                                                                                                              screening assay osteoarthritis;
                                                                                                                      ADJ70433 standard; protein; 1480 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fahy ED, Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2002; 2002US-0372843P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2003; 2003WO-US010870.
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BUCK-) BUCK INST AGE RES
                                                                                                                                                                                                                                                                                Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-845369/78.
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1480 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                      ADJ70433;
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12;

Gaps

80;

Conservative

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1074 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP 1133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
PHQAAAPVD---QTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSAS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; enocional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otsuki T;
                                                                     --SSAVEPVCGDA-APACLLRTPLRGLL
                                                                                                                                               90 KPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein useful for treating neurological disease Seg 3264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T, Isono Y,
Irie R;
                                                                                                                                                                                                                                                                                                                                  1241 PLPSPASTOTL -- ALAPALAPTLGGSS 1265
                                                                                                                                                                                                                                                                                                 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
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                                                                                                                                                                                                                       ---POPLMRTPAARSHWPIP--HPCDT-
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Nagai K, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Wakamatsu A, Ishii S,
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                                                                         A-AAGIA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tranquiliser.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1447413-A2
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(INCY-) INCYTE GENOMICS INC.

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as well as for maintaining equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic and tranquiliser activities. This polypeptide is a protein encoded by a full length human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis; cancer; call proliferative disorder; autolimune disorder; inflammatory disorder; infection; hormonal disorder; metabolic disorder; neurological disorder; dastrointestinal disorder; transport disorder; connective tissue disorder; drug screening; protecome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; knock in; disease model; toxicological testing; transcript imaging;
                                                                                                                                                                                                                                                                                                         -----SSAVEPVCGDA-APACLLRTPLRGLL 89
                                                                                                                                                                                                                                                                                                                             1504 ALTIGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPPSAP
                                                                                                                                                                                                                                                                                                                                                                                          2 PHOAAAPVD----QTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSAS
                                                                                                                                                                                                                                                                                                                                                                       90 KPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ---PQPLMRTPAARSHWPIP--HPCDT-----ACPAPLPVVLVAPRST-----
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                             80;
                                                                                                                                                                          13.6%; Score 154; DB 8; Length 2427; 25.7%; Pred. No. 0.0058; ive 27; Mismatches 92; Indels 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1671 PLPSPASTQTL---ALAPALAPTLGGSS 1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 -ILSMSRIWICRRWAVAPCRAEKLMCSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR41356 standard; protein; 2735 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DITHP transcription factor.
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2001US-0291849P.
2001US-0299428P.
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2001US-0280068P.
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                                                                                                                                                                                                           69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                        59 A-AAGIA-----
                                                                                                                                                                                                                                                                                                                                                                                                    1564 NPAPAQASLLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease model; toxico
transcription factor.
                                                                                                                                                                                            Local Similarity
                                                                                                                                            Sequence 2427 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200297031-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2001;
29-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-2001;
20-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2002;
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The invention relates to novel human diagnostic and therapeutic

CD polymucleotides designated dithp (ACC46080-ACC46749) and to their encoded

CC proteins (DITHP, ABRAH181-ABRAH1812). The invention also relates to

CD polymucleotide sequences at least 90% identical to the dithp cDNA

CC polymucleotide sequences at least 90% identical to the dithp cDNA

CC ransgenic organisms comprising dithp nucleic acid sequence; the

CC recombinant production of DITHP proteins; antibodies specific for DITHP

CC proteins; microarrays comprising dithp nucleic acid sequences; methods of

CC detecting dithp nucleotide and protein sequences; methods of sessing the toxicity of test compounds using a dithp hybridisation

CC diagnosis of a wide variety of conditions including cancer and other cell

CC diagnosis of a wide variety of conditions including cancer and other cell

CC diagnosis of a wide variety of conditions including cancer and other cell

CC disorders; neurological disorders; gastrointestinal disorders; transport

CC disorders; neurological disorders; gastrointestinal disorders; transport

CC disorders; and connective tissue disorders . They may also be used to

CS creen for modulators of protein activity or gene expression. DITHP

CC creen for modulators of protein activity or gene expression. DITHP

CC creel type and to induce antibodies. The dithp nucleic acids are

CC additionally useful in semation and indiported as a source of antisense sequences, as a source of antisense sequences.

CC prober and proposed and protein activity or gene therapy of the disorders in proposed and primers, and antisense sequences. The disorders in the disorders in prober and primers and primers and primers and primers.

CC prober and primers are as source of antisense sequences, as a source of antisense sequences.
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| PAPASAPLTIPISAPLTVSASG----PALLTSVTPPLAPVVPAAPGPPSLAPSGASPSAS 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1009 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1116 VLAPSPGAAPVLASSQTPVPVWAPSSTPGTSLASASPVPAPTPVLAPSSTQTMLPAPVPS 1175
                                                                                                                                                                                                                                                                                               identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a DITHP protein which has transcription factor activity. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formatirectly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the generation of transgenic animal models of human disease or knock in humanised animals, in toxicological testing, and in transcript imaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PHQAAAPVD----QTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---SSAVEPVCGDA-APACLLRTPLRGLL
                                                                                                         EH;
                                                                                                                                                                                                                                                                                       Novel human diagnostic and therapeutic polypeptide useful for identitest compound which specifically binds to a polypeptide encoded by hidagnostic and therapeutic polynucleotide, and to induce antibodies.
                                 Jnes AL, Tran AB, Dahl CR, Gietzen L, L. L. Yu JY, Tuason O, Yap PE, Amshey SR; C, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin F David MH, Lewis SA, Chen AJ, Panzer SR, Harris B; Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 KPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%; Score 154; DB 6; Length 2735; 25.7%; Pred. No. 0.0066; cive 27; Mismatches 92; Indels 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 ---PQPLMRTPAARSHWPIP--HPCDT----ACPAPLPVVLVAPRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1176 PLPSPASTOTL---ALAPALAPTLGGSS 1200
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                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 891; 591pp; English.
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                                                    Daffor.,
Dufour GE, Hillman.
Daughtery SC, Dam TC,
TH David MH,
                                                                                                                               Peralta CH, David MH
Flores V, Marwaha R,
                                                                                                                                                                                                          WPI; 2003-129518/12.
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Matches
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipsoriatic; antiparkinsonian; nootropic; neutroprotective; osteopathic;
anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive;
dermatological; immunosuppressave; antiinflammatory; antibacterial;
antiviral; antifungal; antirhewmatic; antithyroid; and antianaemic. The
sequences can be used for determining the presence of or predisposition
to, or preventing or treating pathological conditions associated with an
ORFX-associated disorder. The nucleic acids can be used to express ORFX
proteins in gene therapy vectors. The proteins and nucleic acids may be
used to treat cancers, proliferative disorders, neurodegenerative
disorders opercontritis, graft vs host disease, cardiovascular disease,
catorage, systemic lupus erythematosus, severe combined immunodeficiency
(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
cationage anneal antiques and manages, noncturnal haemoglobinuria, antiinflammatory disease; to
enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                          vulnezary; antipsoriatic; antiparkinsonian; notropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosupressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotrension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; alleryy; aplastic anaemia; nocturnal haemoglobinutia; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                            Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading frame X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating e.g. cancers, proliferative disorde
neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                Human ORFX ORF995 polypeptide sequence SEQ ID NO:1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 1510-1517; 5507pp; English.
                                            AAB41231 standard; protein; 2971 AA.
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99US-0127636P.
99US-0127728P.
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                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thrombosis; contraceptive.
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02-APR-1999;
05-APR-1999;
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                                                                                                                                   08-FEB-2001
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                                                                                         AAB41231;
RESULT 12
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12;
                                                                                                                                                                                                                                                      The invention describes a method of diagnosing breast cancer in subject comprising contacting biological sample from subject with at least two different breast cancer-associated polypeptides (I) encoded by nucleic acid molecules (II) comprising sequence chosen from 42 fully defined sequences as given in specification, determining specific binding between (I) and agents in sample, where presence of the binding is diagnosing breast cancer. The method is useful for diagnosing breast cancer in a subject. The sample is blood, lymph node fluid or breast discharge fluid. This is the amino acid sequence of a breast cancer antigen.
                                                                                                                              1189 PAPASAPLTIPISAPLTVSASG----PALLTSVTPPLAPVVPAAPGPPSLAPSGASPSAS 1244
                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing breast cancer in subject by obtaining biological sample from subject, contacting sample with breast cancer-associated polypeptides, determining specific binding between polypeptides and agents in sample.
                                                                                                                                                                                                  1245 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP
                                                                                                                                                                   -----SSAVEPVCGDA-APACLLRTPLRGLL
                                                                                                 2 PHQAAAPVD---QTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSAS
                                                                                                                                                                                                                                   90 KPTGPRSTMECPPALIVHPPAGGMASGSSOPWAAASATPMLSSKASLCIPTRGPP----
                                                                 Gaps
                                                                80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast cancer; breast cancer diagnosis; breast cancer antigen.
                             13.6%; Score 154; DB 3; Length 2971; 25.7%; Pred. No. 0.0072; ive 27; Mismatches 92; Indels 80
                                                                                                                                                                                                                                                                                                     145 ---PQPLMRTPAARSHWPIP--HPCDT----ACPAPLPVVLVAPRST-
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                                                                                                                                                                                                                                                                                                                                                                                          183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
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                                                                 69; Conservative
                                                                                                                                                                   59 A-AAGIA------
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                               Query Match
Best Local Similarity
Sequence 2971 AA;
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AAB50362
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                                                                                                                    1245 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP 1304
                                                                                                                                                                ------ASSASQALATPLA-PMAAPQTAILAPSPAPPLAPLP 1351
                                                                                                                                                                                                          1352 VLAPSPGAAPVLASSQTPVPVMAPSSTPGTSLASASPVPAPTPVLAPSSTQTMLPAPVPS 1411
                                12;
                                                                                                                                           144
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                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snf2 related cAMP regulatory element (CREB) binding protein (CBP) activator protein, capable of co-activating CREB binding protein, useful for modulating transcription and for affecting viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is an Snf2 related CREB (cAMP regulatory element) binding protein (CBP) activator protein (SRCAP) polypeptide. It has ATPase activity and is capable of activating transcription. SRCAP polypeptides are useful for activating transcription in a cell, for enhancing CREB (cAMP regulatory element) binding protein (CBP)-mediated activation of transcription in a cell, for treating a patient having a disease involving a function such as insufficient transcription of a gene, e.g. a gene mediated by CBP co-activation, DEAD box RNA dependent
                                                                 Human; SRCAP; Snf2 related CBP activator protein; antiviral; CREB; cAMP regulatory element; CREB binding protein; CBP; ATPase; transcription activation; DEAD box RNA dependent helicase; adenoviral DBP protein; beta-actin; nuclear receptor; viral infection.
                                                   PHQAAAPVD---QTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSAS
                                                                                               A-AAGIA-----SAVEPVCGDA-APACLLRTPLRGLL
                                                                                                                                                                                      ---PQPLMRTPAARSHWPIP--HPCDT-----ACPAPLPVVLVAPRST-----
                                                                                                                                          KPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP----
                                Gaps
                                80;
         Length 2971;
                               Indela
                             92;
         13.4%; Score 152; DB 7; 25.7%; Pred. No. 0.01; ive 27; Mismatches 92;
                                                                                                                                                                                                                                              - ILSMSRTWTCRRWAVAPCRAEKLMCSS
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25-MAY-2000; 2000US-00579181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2000; 2000WO-US014719
      Query Match
Best Local Similarity 25.7*
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYSL-) UNIV SAINT LOUIS.
                                                                                                                                                               1305 NPAPAQASLLAP
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N-PSDB; AAC89860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                             Human SRCAP
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1189 PAPASAPLTIPISAPLTVSASG----PALLITSVTPPLAPVVPAAPGPPSLQPSGASPSAS 1244
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helicase, adenoviral DBP protein, beta-actin or a nuclear receptor affected by SRCAP protein. Compounds that modulate SRCAP function, such as antibodies, antiseanse molecules, polynuclecides or ribozymes, are useful to treating diseases mediated by SRCAP-activated transcription, for example, infection by adenovirus, hepatitis C virus, human immunodeficiency virus type-1, Epstein Barr virus, cytomegalovirus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; SRCAP; Snf2 related CBP activator protein; antiviral; CREB; cAMP regulatory element; CREB pinding protein; CBP; ArPase; transcription activation; DRAD box RNA dependent helicase; adenoviral DBP protein; beta-actin; nuclear receptor; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SSAVBPVCGDA-APACLLRTPLRGLL
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                                                                                                                                                                                                                                                                                                    4; Length 2972;
                                                                                                                                                                                                                                                                                                                                                        92; Indels
                                                                                                                                                                                                                                                                                                 13.4%; Score 152; DB 4
25.7%; Pred. No. 0.01;
ive 27; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB50362 standard; protein; 3118
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25-MAY-2000; 2000US-00579181.
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N-PSDB; AAC89859.
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                                                                                                                                                                             hepatitis B virûs
                                                                                                                                                                                                                                          Sequence 2972 AA;
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The present sequence is an Shf2 related CREB (CAMP regulatory element)

binding protein (CBP) activator protein (SRCAP) polypeptide. It has
Alpase activity and is capable of activating transcription. SRCAP

Alpase activity and is capable of activating transcription in a cell, for

enhancing CREB (CAMP regulatory element) binding protein of activation of transcription in a cell, for treating a patient having a

activation of transcription in a cell, for treating a patient having a

disease involving a function such as insufficient transcription of a

gene, e.g. a gene mediated by CBP co-activation, DEAD box RNA dependent

helicase, adenoviral DBP protein, beta-actin or a nuclear receptor

affected by SRCAP protein. Compounds that modulate SRCAP function, such

as antibodies, antisense molecules, polymucleotides or ribozymes, are

useful for treating diseases mediated by SRCAP-activated transcription,

for example, infection by adenovirus, hepatitis C virus, human

immunodeficiency virus type-1, Epstein Barr virus, cytomegalovirus or X88888888888888888888888888888888888

Sequence 3118 AA;

Query Match
13.4%; Score 152; DB 4; Length 3118;
Best Local Similarity 25.7%; Pred. No. 0.011;
Matches 69; Conservative 27; Mismatches 92; Indels 80

2 PHQAAAPVD----QTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSAS

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A-AAGIA-----SSAVEPVCGDA-APACLIRTPLRGIL 89 29

90 KPTGPRSTMECPPALIVHPPAGGMASGSSQPWANASATPMLSSKASLCIPTRGPP---- 144

1498 VLAPSPGAAPVLASSQTPVPVWAPSSTPGTSLASASPVPAPTPVLAPSSTQTMLPAPVPS 1557 ----PQPLMRTPAARSHWPIP--HPCDT-----ACPAPLPVVLVAPRST------145

183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209

Search completed: March 16, 2006, 15:52:29 Job time : 191 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

Run on:

March 16, 2006, 15:52:45; Search time 40 Seconds (without alignments) 509.949 Million cell updates/sec

US-09-989-890-238 1134 1 SPHQAAAPVDQTPRTLATMG........RRWAVAPCRAEKLMCSSSRS 212 Title: Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

**************************************	SUMMAKLES	Length DB ID Description	2 T48814	2 P75477 hypothetical	2 T49385 hypothetical	1 WMBEH6 UL36 protein	1 I38902	2 A47283	2 T43556	T38819	2 A47282	2 S49915 extensin-like pr	2 A40670	1 QQBE8	T43481	2 G86292	2 T44768	2 I49444	T36729	2 T29018	2 A55617 masquerade p	2 I84499	C41132	2 T05857	2 T38236 hypothetical	2 H96711	2 T46707 proteophospho	2 T04859	1299 2 T47182 hypothetical prote	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
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high molecular mas	gene LF3 protein -	probable ABC trans	hypothetical prote	gag-abl polyprotei	hypothetical prote	hypothetical prote	kinase-related tra	protein BRG1 - hum	SNF2beta protein -	SEC31 protein - ye	hypothetical prote	immediate-early pr	ALR protein - huma	mucin 7 precursor,	hypothetical prote
T18535	\$27923	T35192	F75518	FOMVGM	T04462	D85383	A39962	839059	845252	S58782	F84643	EDBE11	T03454	A48018	T27051
7	~	N	0	н	N	N	~	7	0	7	7	-	0	7	N
1151	924	744	839	981	1008	1069	1123	1613	1647	1273	742	775	5262	377	476
10.3	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.1	10.1	10.1	10.1	10.1	10.1	10.0	10.0
116.5	116	115.5	115.5	115.5	115.5	115.5	115.5	115	115	114.5	114	114	114	113.5	113
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

KESOTI I
T48814
hypothetical protein 15E6.220 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence revision 05-May-2000 #text change 09-Jul-2004
C;Accession: T48814
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, April 2000
A; Reference number: Z24541

A; Accession: T48814

A;Status: preliminary
A;Molecule type: DNA
A;Esperimental tource: cosmid contig 15E6; strain 74
C;Genetics:
A;Gene: NGSP:15E6.220
A;Map position: 2
A;Introns: 281/3

ģ Gaps 43; 13.6%; Score 154.5; DB 2; Length 1952; 30.7%; Pred. No. 0.01; tive 20; Mismatches 77; Indels 43; Query Match Best Local Similarity 30.7% Matches 62; Conservative

22 1 SPHOAAAPVDQT-PRTLATMGQRALP----SSLALLSRPLSPPPAACSGDPGCGSGAGLP 셤 Š

56 SASAAAGIASSAVE--PV-CGDAAPACLIR---TPLRGLLXP-----TGPRSTMECP-- 101 셤 ò

102 -----PALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPPQPLMRTPAAR 155 ò

156 SHWPIPHPCDTACPAPLPVVLV 177 g Š

1923 РРРРРРРРАВАРРРРРТРІМ 1944 d

RESULT : F75477

hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: F75477
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

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A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A;Residues: 1-1721 aBNY2>
A;Residues: 1-1721 aBNY2>
A;Residues: 1-1721 aBNY2>
A;Cross=references: UNIPARC:UPI00001740E0; EMBL:U17838; NID:g1669774; PIDN:AAC50820.1; P
A;Cross=references: UNIPARC:UPI00001740E0; EMBL:U17838, release 114.0, PIDN:AAC50820.1
R;Shapiro, V.S.; Lee, P.; Winoto, A.
Gene 163, 329-330, 1995
A;Title: Identification and cloning of the G3B cDNA encoding a 3' segment of a protein b
A;Reference number: PC4095; MUID:96011660; PMID:7590293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 161-165,'T',167-197,'S',199-201,'G',203-277,'VGGGGGVVVVVSWKARGE',296-308,'SC
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C; Species: Homo sapiens (man)
C; Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text_change 31-Dec-2004
C; Accession: 138902, A59221; FC4095
R; Buyse, I.M.; Shao, G.; Huang, S.
R; Buyse, I.M.; Shao, G.; Huang, S.
A; Huang, S.
A; Huang, S.
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A; Atocasion: 138902
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A; Accession: A; Accession
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                                                                                                                                                                                           NIC
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75477
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residus: 1-635 «WHI>
A;Cross-references: UNIPROT:Q9RW96; UNIPARC:UPI00000C1804; GB:AE001932; GB:AE000513; IA;Experimental source: strain R1
A;Genetics:
A;Genetics:
A;Gene: DR0773
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 GAGONTGASRPASGIPSRASAPNVVVRPPARVSGISAAGAIGSSRIGAAGIPA----A 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPLRGLLKPTGPR-STMECPPALIVHPPAGGM---ASGSSQPWAAASATPMLSSKASL-- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 AAAPLOYPVPYTATPTPPVIPGA------VPPPPQVPGGRP------PSALAVAGPS 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 QPWAAASA----TPMLSSKASLCIPTRGPPQQPLMRTPAARSHWPIPHPCDTACPAPL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAAGIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SASAAAGIASSAVEPVCGDAAPACLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           378 AGAGGALSIDSLFGQGALAALLAGATRKSATPTPSQTGTPQPPIATPIPPPAVPPVAGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVVRPPVPVSGQQPPRVVTSPAAGV-----PAGNAAPAPTPPPVVAAR 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----CIPTRGPPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAPR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SPHQAAAPVDQTPRTLATMGQRALPSSLA----LLSRPLSP--PPAACS---
                                                                                                                                                                                                                                                                                                                                                                                                     Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 11.9%; Score 135.5; DB 2;
1 Similarity 27.6%; Pred. No. 0.079;
54; Conservative 24; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                     12.0%; Score 136.5; DB 2; 26.6%; Pred. No. 0.055; tive 29; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVVLVAPRSTILSMSR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPAPVSNPSALLAMLR 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 61; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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Matches
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Unide protein - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Species: a.1-6c-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: 130085
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Pern J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: 130085
A;Accession: 130085
A;Accession: 130085
A;Cross-references: UNIPROT:P10220; UNIPARC:UP10000136898; GB:X14112; NID:g1944536; PIDN A;Residues: 1-3164 «MCG>
C;Genetics:
A;Cross-references: UNIPROT:P10220; UNIPARC:UP10000136898; GB:X14112; NID:g1944536; PIDN C;Genetics:
A;Gene: UL36
C;Superfamily: varicella-zoster virus gene 22 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2831 GRNPAEPTSSPAGPSPPPPAVQPVAPPPTSGPPPTYLTLEGGVAPGGPVSRRPTTRQ-- 2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2651 SPOSSPAPPDATAPRPPASSRASASSSGSRARRHRRARSLARATOASATTOGWRPPALP 2710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----PMLSSKAS------LCIPTRGPPQ-------PLMRTPAARSHW 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2771 LPGGENRRPPLTSGPAPTPPRVPVGGPQRRLTRPAVASLSESRESLPSPWDPADPTAPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 SSLALL---SRPLSPPPAACSGDPGCGSGAGLPSASAAAGIASSA--VEPVCGDAAPACL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-----QPWAAASAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PRTLA-----TMGOR--ALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 135; DB 1; Length 3164;
; Pred. No. 0.29;
17; Mismatches 86; Indels 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVATPTTSARPRGHLTVSRLSAPOP 2913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SPHQAAAPVDQT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIPHPCDTACP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159
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A;Cross-references: UNIPROT:036027; UNIPARC:UPI00006C8BB; EMBL:298980; NID:e1060691; P. A;Experimental source: strain 972h-; cosmid c4F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-574 <ZANA:
A;Kesidues: 1-574 <ZANA:
A;Cross-references: UNIPROT:036027; UNIPARC:UPI000003CA2E; EMBL:AF038575; PIDN:AAB92587
A;Experimental source: strain JS21
                                                                                                                                                                                                                                                                                                                                             C;Accession: T43556
R;Zankel, T.C.; Ow, D.W.
submitted to the EMBL Data Library, December 1997
A;Description: A Wiskott-Aldrich Syndrome protein homolog in Schizosaccharomyces pombe, A;Reference number: Z22575
A;Accession: T43556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wiskott-aldrich syndrome protein homolog 1 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                             Wiskott-Aldrich syndrome protein homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 ECPPAL----IVHPPA----GGMASGSSQPWAAASAT-----PMLSSKASLCIPT 140
                                                  -----AVAPVV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 NGSSNSSLPPPPPPPPRSNAAG---SIPLPPQGRSAP------PPPPPRSAPSTG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 ROPPPLSSSRAVSNPPAPPPALPGRSAPALPPLGNASRTSTPPVPTPPSLPPSAPPSLPP 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 RGPPPQPLMRTPAA------RSHWPIPHPCDTACPAPLPVVLVAPRSTILSMS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPPSLP-MGAPAAPPLPPSAPIAPPLPAGMPAAPPLPPAAPAPPPAPAPAPAAPVASIA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38819
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPPRPIAPVSMNPAINST-SKPPLPPSSRVSAAALAANKKRPPPPPPPSRRNRGKPPIG
  ---LVAPRSTILSMSRTWTCRRWAVAPCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGAG-----LPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPR---STM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SPHOAAAPVDOTPRILATMGORALP----SSLALLS---RPLSPPPAA--CSGDPGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , 0.099;
82;
                             11.6%; Score 132; DB 2; 28.3%; Pred. No. 0.099; rative 20; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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A,Molecule type: DNA
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Pred. No. 0.099;
  TP---AARSHWPIPHPCDTACPAPLPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%;
28.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 28.39 hes 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 72/3; 519/3; 564/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 72/3; 519/3; 564/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: Z21813
A;Accession: T38819
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Best Local Similarity
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                                                                                                  AE 203
                                                                                                                                                     AE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: I
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  151
                                                                                                     202
                                                                                                                                                     211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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A;Gene: wsp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Genetics:
  ò
                                          셤
                                                                                                  δ
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calphotin - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: A47283

R;Ballinger, D.G; Xue, N.; Harshman, K.D.

Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993

A;Title: A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and A;Reference number: A47283; MUID: 93165730; PMID: 8434015

A;Corents: photoreceptor cells

A;Accession: A47283

A;Accession: A47283

A;Accession: A47283

A;Reference: uncleic acid

A;Molecule type: mucleic acid

A;Residues: 1-873 * RALL

A;Coss-references: UNIPROT: 002910; UNIPARC: UPI000016BB46; GB: L05080; NID: 9157071; PIDN: A;Coss-reference extracted from NCBI backbone (NCBIN: 124958, NCBIP: 124959)

C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
Cross-references: UNIPARC:UP1000007377B; GB:U23736; NID:g915214; PIDN:AAA87023.1; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944 TPDVC-PSSPA--LQTPSLSSGQLPPLLIPTDPSSPPPCPPVLTVATPPPPLLPTVPLPA 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   890 MIQKVILINEYNGIDLPVENPADGTRSPSPCKSLEAQPDPDLGPGSGFPAPTV----ES 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VEPVCGDAAPACLIRTP-----LRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQPW 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
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Best Local Similarity 28.3%; Pred. No. U.1s;
Matches 54; Conservative 21; Mismatches
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                                          A Gene: GDB:RIZ; G3B
A, Cross-references: GDB:636678; OMIM:601196
A, Map Position: 1p36.23-1p36.13
C, Superfamily: SH3 homology
C, Keywords: zinc finger
C, Keywords: zinc finger
C, F34-384/Region: zinc finger CCHH motif
F, 394-414/Region: zinc finger CCHH motif
F, 187-508/Region: zinc finger CCHH motif
F, 1139-1159/Region: zinc finger CCHH motif
F, 1139-1159/Region: zinc finger CCHH motif
F, 1138-1159/Region: zinc finger CCHH motif
F, 1138-1158/Region: zinc finger CCHH motif
F, 11460-1181/Region: zinc finger CCHH motif
F, 11460-1481/Region: zinc finger CCHH motif
F, 1460-1481/Region: zinc finger CCHH motif
                                                                          OMIM: 601196
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A;Status: preliminary
A;Molecule type: DNA
A;Redidues: 1-1188 «KUB»
A;Cross-references: UNIPROT:Q41805; UNIPARC:UPI00000A1616; EMBL:Z34465; NID:g600117; PID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: human herpesvirus 4, Epstein-Barr virus
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C;Accession: G92065; A0374; S22993
K;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BPLF1 protein - human herpesvirus 4 (strain B95-8)
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26.4%;
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Best Local Similarity
Matches 55; Conserv
                                                                                                                                  Query Match
Best Local Similarity
Matches 54; Conserv
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A; Accession: S49915
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Accession: 47282
R; Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993
A; Title: Calphotin: a Drosophila photoreceptor cell calcium-binding protein.
A; Reference number: A47282
A; Accession: A47282
A; MUD: 93165729; PMID: 8094559
A; Accession: A47282
A; Molecule type: nucleic acid
A; Residues: 1-865 c.MAR>
A; Cross-references: UNIPROT: Q02910; UNIPARC: UPI00001282D3; GB: L02111; NID: g157031; PIDN: A; Experimental source: photoreceptor cells
A; Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIP:124956)
C; Genetics:
A; Genetics:
A; Gross-references: FlyBase: FBgn0010218
C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
C; Keywords: calcium binding
13;
                                                                                       270 SPPRPIAPVSMNPAINST-SKPPLPPSSRVSAAALAANKKRPPPPPPPPSRRNRGKPPIG 328
                                                                                                                                                                                                                            ECPPAL----IVHPPA----GGMASGSSQPWAAASAT-----PMLSSKASLCIPT 140
                                                                                                                                                                                                                                                          434 SAPPSLP-MGAPAAPPLPPSAPIAPPLPAGMPAAPPLPPAAPAPAPAPAPAPAPAPAPAAPAAPVASIA 492
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C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Species: OS-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49915
R;Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
submitted to the RMBL Data Library, June 1994
A;Description: Pex genes: pollen-specific genes with extensin-like domains.
A;Reference number: S49915
                                            1 SPHQAAAPVDQTPRTLATMGQRALP----SSLALLS---RPLSPPPAA--CSGDPGCG
                                                                                                                                      SGAG-----LPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPR---STM
                                                                                                                                                                                                                                                                                                                      141 RGPPPQPLMRTPAA------RSHWPIPHPCDTACPAPLPVVLVAPRSTILSMS
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Gaps
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70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 131; DB 2; Length 865
26.6%; Pred. No. 0.17;
tive 23; Mismatches 82; Indels
Indels
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82;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 26.6%
nes 62, Conservative
Conservative
68;
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Best Local S:
Matches 62,
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cibate: 03-May-1994 #Bequence_revision 03-May-1994 #text_change 09-Jul-2004
Cisaccession: A40670
R.Hallberg, E.; Wozniak, R.W.; Blobel, G.
J. Cell Biol. 122, 513-521, 1993
J. Title: An integral membrane protein of the pore membrane domain of the nuclear envelop A, Reference number: A40670; MulD:93328754; PMID:8335683
A, Accession: A40670
A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1199 <HAL>
A;Cross-references: UNIPROT:P52591; UNIPARC:UP1000012FCOE; GB:Z21513; NID:g396746; PIDN:
F;803-807,845-849,956-960,1010-1014,1047-1051,1076-1080/Region: pentapeptide motif (X-F-
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                                                                                                                                                                                                                                                    52 AGLPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAG 111
                                                                                                                                                                                                                                                                                                                                                                                  112 GMASGSSQPWAAASATPMLSSKASLCI----PTRGPPPQPLMRTPAARSHWPIPH---- 162
                                                                                                                                                                                                                                                                                                                                                                                                                         TPATDISPATSPPFILILPIVGPAASPASLPAPSSNPLLESLKKMQESPAPSSSEPPEAA 594
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                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nuclear envelope protein POM 121 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
                                                                                                                                                                                     SPPO--APVGSPPPPVKTTSPPAPIGSPSPPPPVSVVSPPPPVKSPPPPAPVGSPPPPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SPHQAAAPVDQTP--RTLATMGQRALPSSL-ALLSRPL-----SPPPAACSGDPGCGS
                                                                                                                          1 SPHQAAAPVDQTPRTLAT-----MGQRALPSSLALLSRP---LSPPPAACSGDPGCGSG
                                                                                                                                                                                                                                                                                                                   565 SPPPPAPVA----SPPPPVKSPPPTLVASPPPPVKSPPPAPVASPPPVKSPPPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595 TVAAPSPPKTPSLLAPLVSPLTG-------PLASTSSDSKPTTTFL------
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                                                              35;
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                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71,
                                                              66
   DB 2;
11.4%; Score 129.5; DE ilarity 25.8%; Pred. No. 0.28; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 129.5; DE; Pred. No. 0.28; 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 -----PCDTACPAPLPVVLVAPRST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSPPPEKSLPPPTLIPSPPPGEKPTPPST 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHWPIPHPCDTACPAPL -- PVVLVAPRS 181
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antifreeze glycopeptide AFGP polyprotein precursor [imported] - Boreogadus (Species: Boreogadus saida (Species: Boreogadus saida (Species: Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004 (Stacession: T44768 A.L.; Cheng, C.H.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 ----VHPP----AGGMAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489 RIPSRASLIMIPSRAS 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 VAPCRAEKLMCSSSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.0%
Local 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Map position: 1
                                                                                                         35
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                                        267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable mucin DKPZp434C196.1 - human (fragment)
N.Alternate names: protein DKPZp434G0655.1
N.Alternate names: protein DKPZp434G0655.1
C.Species: Homo sapiens (man)
C.Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 09-Jul-2004
C.Accession: T43481; T34549; T17264
R.Kochrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A.Recenter unmber: 222514
A.Accession: T43481
A.Molecule type: mRNA
A.Residues: 1-580 cAAA
A.Residues: 22554
A.Residues: 22558
A.Residues: 2258
A.Residues: 22558
A.Residues:
A; Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus A; Reference number: A93065; MUD:85035713; PMID:6092825
A; Accession: G93065
A; Molecule type: DNA
A; Residues: 1-3149 < BAN>
A; Cross-references: UNIPROT:P03186; UNIPARC:UPI000000CDC7; EMBL:V01555; NID:g59074; PIDN Ribacr. R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Hitle: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A; Reference number: A03794; MUD:84270667; PMID:6087149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 DQLPRTHVPPHR---PPSAARLPPPVIPIPHQSPPASPTPHPA-----PVSTIAPSVT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 SSAVEPV-----CGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMASG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 PSPRLPLQIPIPLPQAAPSNPKIPLTTPSPSPTAAAAPTTTTLSPPPTQQQPPQSAAPAP 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S----SQPWAAASATPMLSSKASLCIPTRGPPPQPLMRTPAARSHWPIP---HPCDTAC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  554 SPLLPOQQPTPSAAPAP----SPLLPQQQPPS-----AARAPSPLPPQQQPLPSAT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 DQTPRTLATMGQRALPSSLALLSRPLSP----PPAACSGDPGCGSGAGLPSASAAGIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Note: DKFZp434C196.1; DKFZp434B0635.1; DKFZp434B061.1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.4%; Score 129.5; DB 1; Best Local Similarity 27.0%; Pred. No. 0.65; Matches 53; Conservative 20; Mismatches 80;
                                                                                                                                                                                                                                                                                                                               Contents: annotation; protein coding region Superfamily: human herpesvirus 4 BPLF1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602 PAPPPAQQLPPSATTL 617
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Cjaccesion: G8622

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.; Liu, Z.B.; Lin, Z.B.; Maiti, R.; Fallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: G86592
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A;Residues: 1-1006 <STO> .
A;Cross-references: UNIPROT:Q9LMQ1; UNIPARC:UPI00000A2407; GB:AE005172; NID:g8927662; P!
                                                                                                                                                                                                                                                                                                                                                                                       385 RA-----SLIGIPPRASLIGISSI--ASLIRIQSSSSLIRIPSMASLIRI 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || :| : || :||| SPPRASPMTPPRASPTTTPSRASLTRTPSWASPTTTPSRASLMKMESTVSIT 326
                                                                                                                                                                                                     PPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAPRSTI-----LSMSRTWTCRRWA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyporhetical protein F7H2.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                           LSPPPAACSGDPGCGSGAGLPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGP
                                                                                                                                                                                                                                                                                                                                  95 RSTMECPPALIVHPPAGGMASGSSQPWAAASATP------MLSSKASLCIPTRG
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- Boreogadus saida

34

1 SPHQAA--APVDQTPRTLATMGQRALPSSLALLSRP-------

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Proc. Natl. Acad. Sci. U.S.A. 94, 3817-3822, 1997
A,Title: Convergent evolution of antifreeze glycopeptides in Antarctic notothenioid fish A,Reference number: Z22834; MUID:97268653; PMID:9108061
A,Accession: T4610.
A,Accession: T4610.
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Rosidues: 1-507 <CHE>
A,Rosidues: 1-507 <CHE>
A,Rosidues: 1-507 <CHE>
A,Toross-references: UNIPROT:013028; UNIPARC:UPI00000FD737; EMBL:U43200; NID:g2078482; PIC;Genetics:
A,Introns: 1/3
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                                                                                                                                                                                                                                                                                                                                                                                                                   282 ATAATDATAATAATAARAATPATAATAATPATAATAATAATAATAATAATAATAARAARAARA 341
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                                                                                                                                                                                                                                                                                                                                        31; Gaps
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.6%; Pred. No. 0.15;
Matches 51; Conservative 23; Mismatches 94; Indels 31.
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Search completed: March 16, 2006, 15:57:09 Job time : 41 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

March 16, 2006, 15:49:24 ; Search time 230 Seconds Run on:

(without alignments) 650.313 Million cell updates/sec

Title: Perfect so Sequence:

score:

US-09-989-890-238 1134 1 SPHQAAAPVDQTPRTLATMG......RRWAVAPCRABKLMCSSSRS 212

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:* Database :

1: uniprot_sprot:* 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

	Description	Q68d65 homo sapien	mus m	Q8c1q5 mus musculu	Q9p6t1 neurospora		homo	O15026 homo sapien	Q6c7q8 yarrowia li	Q9y519 homo sapien	-	Q6cb04 yarrowia li	Q8fm53 corynebacte	Q6n5q1 rhodopseudo	Q4fx85 leishmania	Q4pf94 ustilago ma		Q9h6k5 homo sapien		Q63vc5 burkholderi	Q9p682 neurospora		-		-	Q5thj1 homo sapien	homo	рошо	homo	Q5z2i3 nocardia fa	•	Q4fx64 leishmania
SUMMARIES	ΙD	Q68D65 HUMAN	Q922Q0 MOUSE	Q8C1Q5_MOUSE	Q9P6T1 NEUCR	Q6ZTM8_HUMAN	Q6ZRS2 HUMAN	015026 HUMAN	Q6C7Q8_YARLI	Q9Y5L9_HUMAN	Q8VPM8_9MICC	Q6CB04_YARLI	Q8FM53_COREF	Q6N5Q1 RHOPA	Q4FX85 LEIMA	Q4PF94_USTMA	Q615V3_ORYSA	Q9H6K5 HUMAN	Q9RW96_DEIRA	Q63VC5_BURPS	Q9P682_NEUCR	Q7RY24_NEUCR	CPN_DROME	TEGU_HHV11	Q6TVP0_9POXV	QSTHJ1_HUMAN	QSTHJO HUMAN	Q59H82 HUMAN	PRDM2 HUMAN	Q5Z2I3_NOCFA	Q9BKV7_LEIMA	Q4FX64_LEIMA
	BB :	2	~	~	N	~	~	N	0	7	~	N	N	~	~	0	~	~	7	~	~	~	-	Н	~	7	7	~	н	~	~	7
	Query Match Length	207	216	367	1992	559	2427	3053	629	2971	406	780	609	829	1514	546	269	616	635	463	803	817	864	3164	328	1481	1540	1576	1718	475	1325	1435
٠	Query	68.3	60.0	24.5	13.6	13.6	13.6	13.6	13.4	13.4	13.3	12.6	12.3	12.2	12.2	12.2	12.1	12.1	12.0	11.9	11.9	11.9	11.9	11.9	11.9	11.9	11.9	11.9		11.8	11.7	11.7
	Score	775	680	278	154.5	154	154	154	152	-1	150.5	143	139	138.5	138.5	138	137	137	136.5	135.5	135.5	135.5	135.5	135	134.5	134.5	134.5	134.5	134.5	134	133	133
	Result No.	н	7	m	4	S	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

		Q4ln41 burkholderi					Q8uz11 pseudorabie			Q7t591 cercopithec	_	Q4fx62 leishmania	_	
Q60DH6 ORYSA	Q4FX63_LEIMA	Q4LN41 9BURK	Q6K322 ORYSA	Q4VBD6 MOUSE	Q4T2J8_TETNG	Q5PPB8 9ALPH	Q8UZ11 PRVKA	Q9XIV1_CUCSA	WSP1 SCHPO	07T591 CHV1	Q6K1T4 ORYSA	Q4FX62_LEIMA	Q650Z7_ORYSA	
08 2	94 2	83 2	50 2	69 2	65 2	84 2	84 2	43 2	74 1	26 2	90 2	92 2	40 2	
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11.7	11.	11.7	11.	11	11.	11.7	11.	11.6	11.6	11.6	11.6	11.6	11.5	
133	133	132.5	132.5	132.5	132.5	132.5	132.5	132	132	132	131.5	131.5	130.5	
32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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117
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                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, CR749558; CAH18355.1; -; mRNA.

Hypothetical protein.

SRQUENCE 207 AA; 22216 MW; FCGE65C436F28ED7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 PRPASGP----PR----LGPWERPTELCLETYDKPPOPPSRRTRRPDPKDPGHGPESI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.3%; Score 775; DB 2; Length 207; Best Local Similarity 72.6%; Pred. No. 9.3e-41; Matches 156; Conservative 10; Mismatches 31; Indels 1
                                                                                                                                        25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686B17277.
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Last sequence update)
Last annotation update)
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0922007
01-DEC-2001 (TEMBLE1. 19, C)
01-DEC-2001 (TEMBLE1. 19, L,
01-JUN-2002 (TEMBLE1. 21, L,
RIKEN CDNA 1810019516.
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The German cDNA Consortium;
                                                                           QGBD65_HUMAN PRELIMINARY;
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                                                                                                                     Q68D65;
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RESULT 1
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068D65 HU
068D DT 25-0
DT 25-0
DT 25-0
DE Hypo
CO Buka
CO Mamm
CO Homo
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Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa T., Taawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Santo R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suruki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Winniaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Manachi, V., Manachi, V., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/60; TISSUE-Pancreas; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Normalization and Subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE-Pancreas;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUB=Pancreas;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                    Carninci P., Hayashizaki Y.;
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The FANTOM Consortium,
the RIKEN Genome Exploration Resea
                           Muroidea; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Nature 420:563-573(2002).
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
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                                                                                                                                               NUCLEOTIDE
   AEALENTINE SEQUENCE.

OE STRAINE-22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouee L.H., Derge J.G.,

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B Hopkins R.F., Jordan H., Morer T.A., Rubin G.M., Hong L.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

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B Hand M. A., Schein J.E., Jones E.D., M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
library, clone:1810019316 product:SIMILAR TO TATA BOX BINDING PROTEIN
(TBP)-ASSOCIATED PACTOR, RNA POLYMERASE II, C1, 130KD homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WAAASATPMLSSKASLCIPTRGPPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAPR
                                      Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Murinee, Murinee, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SPHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, BC006890; AAH06890.1; -; mRNA.
MGI; MGI:1916323; 1810019416Rik.
SEQUENCE 216 AA; 21683 MW; F7AD1985BC0976D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STILSMSRTWTCRRWAVAPCRAEKLMCSSSRS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STTPSMNRTWTCLRWAVAPCRAGRSTCLFSRS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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AC Q8CIQ5;
DT 01-MAR-2003 (TrEMBLrel. 23,
DT 01-MAR-2003 (TrEMBLrel. 24,
DT 01-JUN-2003 (TREMBLrel. 24,
DE 11-STAND OF STAND OF ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
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   Name=1810019J16Rik;
                                                                                                                                                                                      NCBI_TaxID=10090;
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185

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121

207430 MW; CA84145FD154281B CRC64;

us-09-989-890-238.rup

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1992 AA;
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      SEQUENCE
                                     Query Match
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                                                                                                                                                                                                                                                                                                                        AGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQP 120
                                                                                                                                                                                                                                                                                                                                                                                    121 WAAASATPMLSSKASLCIPTRGPPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAPR 180
                                                                                                                                                                                                                                                                                        64
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatou M., Hayashizaki Y.; Suzuki H., Tagama K., Moshida K., Yoshino M., Submitted (UTL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK007551; BAC25177.1; -; mRNA.
Engembl; ENSKUGS0000003760; Mus musculus.

MGI; MGI:1916323; 181001931681k.

SEQUENCE 367 AA; 38538 MW; D558AD91D04FF473 CRC64;
                                                                                                                                                                                                                                                           1 SPHOAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAA
                                                                                                                                                                                                                                                                             SPHRAVAPGGGTLRTLATTGGRVSPSFQALQNOPTSPQPAASSGAPGVGTGVGLPSASDA
                                                                                                                                                                                                                                                                                                                                             117 DGQRLKTSMGSSFSYPDVKLKGIPVYPYRHATS----PVP-DVDSCCKEP----LAEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Neurospora genome project;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; A1353922; CAB88653.2; -; Genomic_DNA.

R PIR; T48814; T48814; T48814;
R GO; GO:0005534; IKQ9.

R GO; GO:00053700; F:transcription factor activity; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR00165; TF Fork head.

R InterPro; IPR011991; Wing_hlx_DNA_bd.

R Ffan; PF02178; AT_hook.

R Pfam; PF02178; R Fhook ad.

R Pfam; PF02178; R Fhook ad.
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                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                           24.5%; Score 278; DB 2; Length 367; 40.8%; Pred. No. 9.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRZ-2004 (TrEMBLrel. 26, Last annotation update)
01-DRZ-2004 (TrEMBLrel. 26, Last annotation update)
03-05-05-05-05-05-05-05-05-05
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                                                                                                                                                                                                                          17; Mismatches
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PRINTS; PR00055; FORKHEAD.
ProDom; PD000425; TF Fork head; 1.
SMART; SM0384; AT hook; Z.
SMART; SM00339; FH; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                           Local Similarity 40.8% nes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPECTI_NEUCR PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |: |:|
167 PTRHSLPSTFT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 STILSMSRTWT 191
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                                                                                                                                                                                                                                                                                                                        61
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Matches
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1853 APSAAQSVAPAPVSSTPVPAATVAPASTVAAAPTPTRVTAAPAALSAATNPAPVPSQPQH 1912
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                                                                                                                                                                                                                                                                               56 SASAAAGIASSAVE--PV-CGDAAPACLLR---TPLRGLLKP-----TGPRSTMBCP-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 PAPASAPLIIPISAPLIVSASG----PALLISVTPPLAPVVPAAPGPPSLAPSGASPSAS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 ALTLGLÄTAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPÄSALASPFPSAP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 KPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP---- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 NPAPAQASLLAP-----ASSASQALATPLA-PMAAPQTAILAPSPAPPLAPLP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 ---POPLMRTPAARSHWPIP--HPCDT-----ACPAPLPVVLVAPRST----- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 VLAPSPGAAPVLASSQTPVPVMAPSSTPGTSLASASPVPAPTPVLAPSSTQTMLPAPVPS 319
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                                                                                                                                                                                                                                                                                                                                                                                                                    -----PALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPPPQPLMRTPAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                    1 SPHOAAAPVDOT-PRILAIMGORALP----SSLALLSRPLSPPAACSGDPGCGSGAGLP
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                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oca T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T. Irie R., Otguki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Pujii A., Oshima Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Isogai T., Masuho Y., Nagai K., Isogai T., Submitted (JUL-2003) to the BMBL/GenBank/DDBJ databases.

SMBL, AK126463, BA0886558 th; PMRNA.

SRQUENCE 559 AA; 54028 MW; B5550A2AE92BA942 CRC64;
                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
       Length 1992;
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                                                                   77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
       DB 2;
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13.6%; Score 154.5; D
30.7%; Pred. No. 0.2;
ive 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 PLPSPASTOTL---ALAPALAPTIGGSS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1963 PPPPPPPPARAPPPPPTPLM 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 SHWPIPHPCDTACPAPLPVVLV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein FLJ44499.
                                                                           62; Conservative
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                                       Local Similarity
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Best Local Similarity
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R. Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,

R. Kawai B., Sugiyama A., Takemoto J., Isono Y.,

R. Kawai Hio Y., Satto K., Nishikawa T., Kimura K., Yamashita H.,

R. Kawai Hio Y., Sakine M., Kikuchi H., Kanda K., Magateuma M.,

R. Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Magateuma M.,

R. Marsuo S., Nagamari K., Masuho Y., Nagai K., Isogai T.;

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

C. -: Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

G. GO:0005634; F.ATP binding; IEA.

GO: GO:0004366; F.ATP binding; IEA.

GO: GO:0004366; F.helicase activity; IEA.

GO: GO:0004366; F.helicase activity; IEA.

BR GO: GO:0006281; P.NA repair; IEA.

BR Ffam; PPO0721; Helicase C.; 1.

R Ffam; PPO0721; Helicase C.; 1.

R SWART; SMO0487; BSAD:

R SWART; SMO0487; HSA; 1.

SWART; SMO0487; HSA; 1.

SWART; SMO0573; HSA; 1.

SWART; SMO0573; HSA; 1.

SWART; SMO0573; HSA; 1.

SWART; SMO0573; HSA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1504 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP 1563
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                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ46149.
Hymo sapiens (Human)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 A-AAGIA----SAVEPVCGDA-APACLIRTPLRGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PHOAAAPVD---QTPRTLATMGQRALPSSLALLSRPLSPPAACSGDPGCGSGAGLPSAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.6%; Score 154; DB 2; Length 2427; Best Local Similarity 25.7%; Pred. No. 0.26; Matches 69; Conservative 27; Mismatches 92; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2427 AA; 260573 MW; 1BD1BDB747FF5927 CRC64;
                                             PRT; 2427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
                                          QGZRS2 HUMAN PRELIMINARY;
QGZRS2;
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                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Anyajima N., Tanaka A., Kotani H., Nomira N., Ohira M., Seki N.,

Ryajima N., Tanaka A., Kotani H., Nomira N., Ohara O.;

Myajima N., Tanaka A., Kotani H., Nomira N., Ohara O.;

RT The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 4:141-150(1997).

REMBL, ABOUSJOY, BAA20768.2; -; mRNA.

BREMBL, ABOUSJOY, BAA20768.2; -; mRNA.

COG. CO.0004102; F. Histone acetyltransferase activity; TAS.

GO; GO:000412; F. Histone acetyltransferase activity; TAS.

GO; GO:0006357; P: regulation of transcription from RNA polyme. . .; TAS.

INTERPRO; IPRO01651; A-T hook.

INTERPRO; IPRO01652; Helicase C.

INTERPRO; IPRO01565; Helicase C.

INTERPRO; IPRO01565; Helicase C.

INTERPRO; IPRO0159; Helicase C.

INTERPRO; IPRO0159; Helicase C.

INTERPRO; IPRO0159; Helicase C.

INTERPRO; IPRO0159; Helicase C.

INTERPROSOULT; Helicase C.

INTERPROSOULT; Helicase C.

REMBL, PRO0150; Helicase C.

REMBL, PRO0150; Helicase C.

REMBL, PRO0150; Helicase C.

REMBL, PRO0150; SNR2.N.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 KPTGPRSTWECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP---- 144
                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3053 AA; 325778 MW; 721B4861D37E19C2 CRC64;
                                                                                                                                                 Last sequence update)
Last annotation update)
              PRT; 3053 AA
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                                                                                                       Created)
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                                                                                             01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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SMART; SM00384; AT hook; 3.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                               KIAA0309 protein (Fragment)
O15026 HUMAN PRELIMINARY;
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es 69; Conserv
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                                                                                                                                                                                                                                                                                         Name=KIAA0309;
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SEQUENCE
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RESULT 8 Q6C7Q8_YARLI

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Plasmid pSD10
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                                                                                                                                                                                     PubMed=15229592; DOI=10.1038/nature00579;
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Mark C., Neuveglise C., Talla B.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lewiller H.,
Nicaud J.-M., Nikolaki M., Oztas S., Ozter-Kalogeropoulos O.,
Nicaud J.-M., Nikolaki M., Oztas S., Ozter-Kalogeropoulos O.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zandou-Meyer M., Zivanovic Y., Bolctin-Pukuhara M., Thierry A.,
Wincker P., Souciet J.-L.;
Wincker P., Souciet J.-L.;
Mature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AYGAPAPTPGTSSPKPPPK----PAKRPPALKPKRIPTPGLKPAVPTPGQRRSVSPS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SPPOGGAPA--IPSLRKTSGAPSAPGGFA----PPPPPAPPGGAPAIPGAPSVASSYRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AGIASSA-----VEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGM 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 ASASSGAPPPPPGGAPPIPGGAPP-----PLPGKVSTSGGAPTFGAPP---PPPGGAP 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 ASGSSQPWAAASATPMLSSKÄSLCIPTRGPP---PQPLMRTPAARSHWPIP-----HPC 164
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Gaps
                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|Q95JC9 Sus scrofa Basic proline-rich protein.
OrderedLocusNames=MLIOD261919;
Yarrowia lipolytica (Candida lipolytica).
Bukaryota, Pungi; Ascomycota, Saccharomycotina, Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Indels
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Last annotation update)
                                                                                                                                                                            NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 13.4%; Score 152; DB 2
1. Similarity 27.4%; Pred. No. 0.11;
57; Conservative 21; Mismatches
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                                                                                                                                 Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003124; WH2. Pfam; PF02205; WH2; 1.
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Q9Y5L9;
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SEQUENCE 659 AA
                                                                                                                                               NCBI_TaxID=4952;
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1305 NPAPAQASLLAP-----ASSASQALATPLA-PMAAPQTAILAPSPAPPLAPLP 1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 A-AAGIA-----SAVEPVCGDA-APACLLRTPLRGLL
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Zhong Z., Caspi R., Mincer T., Helinski D., Knauf V., Boardman K., Wilkinson J.E., Shea T., DeLoughery C., Toukdarian A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AAK62519.1; -; Genomic_DNA.
MEDLINE=99278407; PubMed=10347196; DOI=10.1074/jbc.274.23.16370; Johnston H., Kneer J., Chackalaparampil I., Yaciuk P., Chrivia J.; "Identification of a novel SNF2/SWIZ protein family member, SRCAP, which interacts with CREB-binding protein."; J. Biol. Chem. 274:16370-16376(1999).

EMBL; AF13946; AAD39760.1; -; mRNA.

FRANSFAC; T04151; -.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004386; F:helicase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 152; DB 2; Length 2971; 25.7%; Pred. No. 0.41; ive 27; Mismatches 92; Indels 80
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR0016517; A+T hook.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR0013010; SNP2_N.
Pfam; PP02178; AT hook; 3.
Pfam; PP02171; Helicase C; 1.
Pfam; PR00176; SNP2_N; 1.
Pfam; PR00176; SNP2_N; 1.
Pfam; PR00184; AT hook; 3.
SWART; SM00494; DEXDC; 1.
SWART; SM00490; HELICC; 1.
SRART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 AA; 38781 MW; 2E233C7D5637398B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Proline-rich extensin-like protein.
Micrococcus sp. 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micrococcineae; Micrococcaceae; Micrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1412 PLPSPASTQTL---ALAPALAPTLGGSS 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 25.7%
Les 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBVPMB_9MICC PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=161213;
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                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26, UNDERFERE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterium efficiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QENSQ1 RHOPA PRELIMINARY;
QENSQ1;
                                                                                                                                                                                                                                                            COREF PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=CE2654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
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es 72; Conserv
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-LRVEEL
                              180 RST 182
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                                                                                               ASS 256
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2668501 RHG
2668501 RHG
AC GENSG
DT 05-JU
DT 05-JU
DE Hypot
GN Order
CO Bacte
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A Lafontaine I., de Montigury J., Marche P., Casaregola S.,
Lafontaine I., de Montigury J., March C., Neuveglise C., Talla E.,
Lafontaine I., de Montigury J., March C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerreet A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Pellenz S., Potier S., Richard G.F., Straub M.-L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic Y., Bolotin-Pukuhara M., Thierry A.,
Mincker C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 P-ASSSAPVSSTTPVSSAAPSSEAPVAANSTTPAASSAAPVSSOATTPLPSSAPANSTAP 253
                                                                                                                                                                                                                                                                                                                            78 ATALLGDAAAIAPAPAGRSAAFFSLAAAEFLAPPATAPFWFTPVWEAFSPDLSFEFRGRT 137
                                                                                                                                                                                                                                                                                                                                                                                             ------PASATPMLSSKASLC----IPT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 PGAAALADWPPAAGATPAAARPAAVPARAPLIGDAPPAAGLTPAPESSPSLASTRSTVPS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 AAGSASEA--PVAANSTSPVASSAP----VSSTTPVSS-TTPVSSVAPSSAVPVASNSTS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 PWAAASATPMLSSKASLCIPTRGPPQQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 PHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSG--AGLPSASA 59
                                                                                                                                                                                           18 SPAAGAAPPUSSGVSTPPDASPAGASSLPEVPAAPPAEDAPAPSPEPDSPPRPETAPAPE 77
                                                                                                                          1 SPHQAAAPVD----QTPRTLATMGQRALPSSLALLSRPLSPPAACSGDPGCGSGAGLPS
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=YALIOC22924g;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to sp|P08640 Saccharomyces cerevisiae YIR019c STA1 extracellular alpha-1.
                                                                                                                                                                                                                                                               57 ASAAAGIASSAVEPVCGDAA--PACLLRTPLR-GLLKPTGPRSTMECP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 RGPPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAPRSTIL 184
                              Pred. No. 0.087;
8; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 143; DB 2; Le 30.1%; Pred. No. 0.45; ive 23; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                             102 ---PALIVHPPAGGMASGSSQPWA-
27.78; 22-
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Matches 55; Conservative
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                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  780 AA;
                           Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4952;
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25-OCT-2004
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AAVPAPATPIPPAAPGSAIPAPGAVTPTAVPTPGAAVPAPATPTPPAAPGSAIPAPGAAT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PP-QPLMRTPAARSHWPIP----HPCDTACPAPLPVVLVAPRSTILSMSRTWTCRRWAVA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAPVDQTPRTLATMGQ-----PALPSSLALLSRPLSPPPAACSGD----PGCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GAGLPSASAAAGIASSAVEPVCGDAAPACILRTPLRGLLKP--TGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                            STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                               Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 13:1572-1579 (2003).
EMBL. BA000035; BAC19464.1; -; Genomic DNA.
Complete proteome; Hypothetical protein.
SEQUENCE 609 AA; 61385 MW; D127080D3874A578 CRC64;
Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%; Score 139; DB 2; L 29.1%; Pred. No. 0.64; ive 18; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            829 AA
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Q4PF947
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            PubMed=14704707; DOI-10.1038/nbt923;
PubMed=14704707; DOI-10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
And M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
Harrison P.H., Gibson J., Harwood C.S.;
Complete genome sequence of the metabolically versatile
T. Potcosynthetic bacterium Rhodopseudomonas palustris.";
Nat. Biotechnol. 22.55-51(2004).
EMBL; BX572602; CAE28364.1; -; Genomic DNA.
RO; GO:0003693; P:caspase activity; IRĀ.
RO; GO:0005698; P:proteolysis and peptidolysis; IRA.
InterPro; IPR011600; Pept. [44, p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678 PSAGSAPKPLAGTPPAGGGPAVRPEAVRP--QQQAPAARLRPTPPVTAPARPAGP---- 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 APAGAAPAVQALPVPGTKGLPPAPGVAARPGIPSVAQPQPQPPGRPALGPGGPAAARNGTVA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 CPPALIVH---PPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPPPQ---PLMRTPA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 -РРАААVDRRPPPAAPRIQRPAPPTVSRPVPPPMHVAPRVAPP---РРРОНААРRМAPPP 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 PGCGSG----AGLPSASAAAGIASSAVEPVCGDAAPACLLR--TPLRGLLKPTGPRSTME 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B700FD96D06B4EA8 CRC64;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome; Hypothetical protein; Signal.
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PubMed=16020728; DOI=10.1126/science.1112680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%; Score 138.5; Di 29.7%; Pred. No. 0.91;
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Matches 62; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 APVDQTP--RTLATMGQRALPSSLALLSRP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         787 APVRAAPPPPHVAPPRPPAP-PRAAPPPR 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential
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RCEACLEGATION SEQUENCE.
RA AIL-ZAHTAM M. Allen T., Abouelleil A., Adekoya B.,
AIL-ZAHTAM M., Allen T., Ah P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantaang P., Baldwin J., Barry A.,
RA Arachchi H., Armbruster J., Balcom T., Blye J., Boguslavskiy L.,
RA Bayul T., Blitshateyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Galvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Clurcon M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA Doride K., Daveris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Firgerald M., Foly K., Gage D., Galagan J., Galaten K., Hafez N.,
R Firgerald M., Poly K., Gage D., Galagan J., Galaten K., Hafez N.,
R Firgerald M., Foly K., Gage D., Galagan J., Galaten K., Haigins H.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
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RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlson E.,
RA Lindblad-toh K., Liu X., Lokyiteang T., Lokyiteang Y., Lucien O.,
Ludders T., Leger J., Levine S., Lewis D., Lewis D.,
Anning J., Marbella R., Maru K., Matchew C., Maucell B.,
Mocarthy M., Mcdonough S., Mcghee T., Mikkelsen T., Melarim J., Manlalev A., Mihova T., Mikkelsen T., Melarim J., Manlalev A., Mihova T., Mikkelsen T., Melarim J., Manlalev A., Wihova T., Nielsen C., Nizzari M., Norbu N., O'donnell P., Okoawo O, O'leary S., Omotosho B.,
Norbu N., O'donnell P., Okoawo O, O'leary S., Omotosho B.,
Retta R., Richardson S., Rasker S., Perrin D., Ray Purcell S., Rachupka T., Ramasamy U., Remeau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rase Retta R., Richardson S., Rettipalli S., Rachupka T., Rawasama C., Settipalli S., Rachupka T., Rawasama C., Settipalli S., Setuppach R., Rutman M., Schupbach R., Rocket S., Rachupka T., Rawasama C., Ray S., Rachupka T., Rawasama C., Settipalli S., Rachupka T., Rawasama C., Settipalli 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 КААРААРААРАА--РААРКААРАА------РААРКААРААРААРААРААРААРААРА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 ASGSSQPWAAASATPM---LSSKASLCIPTRGPPQQPLMRTPAARSHWPIP-----HPCD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 SASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECP--PALIVHPPAGGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SPHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSP-----PPAACSGDPGCGSGAGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 TACPAPLPVVLVAPRSTILSMSRTW--TCRRWAVA--PCRAEKLMCSSSRS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 PAAPKAAPVPPAAP-SVLSAPAVFWRVQSRKGSVAGGSYAAEQRMSSSGSS 509
                                                                                                                                                                                                                                                                                                                                                                                                           33;
Myler P.J.; "The Genome of the Kinetoplastid Parasite, Leishmania major."; Science 309:436-442(2005).
EMBL; CP000081; AAZ14258.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                   Length 1514;
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Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBI_TaxID=237631;
                                                                                                                                                                                                                                                                                                          12.2%; Score 138.5; DB 2; Length 1
27.7%; Pred. No. 1.6;
ive 23; Mismatches 111; Indels
                                                                                                                                                                              Hypothetical protein.
SEQUENCE 1514 AA; 150839 MW; 88663AD628129720 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                      64; Conservative
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ORFNames=UM01219.1;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
Stenten K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
Tenzing P., Tesfaye S., Theodore J., Thouluteang Y., Topham K.,
Towey S., Teamla T., Tsomo N., Vallee D., Vassiliev H.,
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A mangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
Xang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
The genome sequence of Ustilago maydis.";
Submitted (FEB-2004) to the EMBL/Genbank/DDBJ databaee.
C-1- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
C-2 Preliminary data.
C-3 FMBL, AACPO1000043; EAK81826.1; -; Genomic_DNA.
C-3 FMBL, AACPO1000043; EAK81826.1; -; Genomic_DNA.
C-3 FMBL, AACPO1000043; EAK81826.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 WAAASATPMLSSKASLC-----IPTRGPPQ-----PLMRTPAARSHWPIPHPCD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 ATKKRGRPPKNVEASFAAAAIPAAPPTAAEAPQLKKRGRPPKAQTATAQPLVPVQQPF- 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPRACSGDPGCGSGAGLPSASAAAGIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.2%; Score 138; DB 2; Length 546; Best Local Similarity 30.4%; Pred. No. 0.67; Matches 59; Conservative 19; Mismatches 70; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 TACPAPLPVVLVAP 179
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Search completed: March 16, 2006, 15:56:24 Job time : 233 secs

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Sequence 2, Appli
Sequence 1803, A
Sequence 11383, A
Sequence 4, Appli
Sequence 28087, A
Sequence 2243, Ap
Sequence 2534, A
Sequence 25344, A
Sequence 25344, A
Sequence 2798, Ap
Sequence 2798, Ap
Sequence 2798, Ap
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Sequence 2, Appli
Sequence 20408, A
                                                             March 16, 2006, 15:56:40 ; Search time 48 Seconds (without alignments) 365.151 Million cell updates/sec
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                                                                                                                              1 SPHQAAAPVDQTPRTLATMG.....RRWAVAPCRAEKLMCSSSRS 212
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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:: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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:: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
:: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
:: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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S-10-104-047-3402
S-10-104-047-2232
S-10-104-047-2243
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S-09-252-991A-20441
S-09-107-433-2798
S-09-107-433-2391
S-10-104-047-2246
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S-09-949-016-11383
S-08-949-016-11383
S-08-399-411-4
S-08-516-859A-4
S-09-528-472-4
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                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                   572060 seqs, 82675679 residues
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Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
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No.
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Sequence 27781, A Sequence 2, Appli Sequence 26813, A Sequence 4, Appli Sequence 12998, A Sequence 12998, A Sequence 7263, Appl Sequence 7263, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 22, Appl Sequence 25, Appl Sequence	(SRCAP)	2; Length 2972; 92; Indels 80; Gaps 12; 92; Indels 80; Gaps 12; 82; Indels 80; Gaps 12; 82; Indels 80; Gaps 12; 83;
US-09-252-991A-27781 US-09-332-063-2 US-09-332-063-3 US-09-332-063-3 US-09-252-991A-26873 US-09-252-991A-26946 US-09-949-016-9748 US-09-949-016-9748 US-08-949-016-6036 US-08-949-016-6036 US-08-949-016-6036 US-08-9949-016-6036 US-09-993-674A-52 US-09-993-674A-52 US-09-993-016-8269 US-09-252-991A-2545	ALIGNMENTS 09579181 calated CBP Activator Protein vs/09/579,181 05-25 60/136,620	ore 152; DB mismatches Mismatches DRALPSSIALLS LLAPTSSHVPGL LLAPTSSHVPGLASSASONAA HPCDT APSTPGTSLAS APSSTPGTSLAS TLGGSS 1436
10.7 10.7 10.7 10.7 10.7 10.6	ion US/(John Peter SNR24 SNR24 NUMBER 1999-01 1999-01 S: 17	milarity Conserva Conserva HQAAAPUD APASAPLTIP
28 121.5 30 121.5 31 121.5 32 120.5 34 120.5 35 120.5 36 120.5 37 120.5 38 120.5 40 120 40 120 41 120 42 120 44 118.5	RESULT 1 US-09-579-181-2 ; Sequence 2, Applicati ; Patent No. 6365372 ; GENERAL INFORMATION: ; APPLICANT: Chrivia, APPLICANT: Chrivia, ; TITLE OF INVENTION: ; FILE REFERENCE: 161 ; CURRENT APPLICATION: ; FILE REFERENCE: 161 ; CURRENT APPLICATION ; FILE OF THING DATE: ; NUMBER OF SEQ ID NOS ; SOFTWARE: PATENTING DATE: ; NUMBER OF SEQ ID NOS ; SOFTWARE: PATENTING ; SEQ ID NO 2 ; TENGTH: 2972	Query Match Best Local Si Matches 69; QY 2 P Db 1189 P QY 59 A QY 90 K Db 1305 N QY 145 - Db 1352 V QY 145 - Db 1352 V CY 145
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Sequence 11382, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHIGMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: LOLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: RESECTED NOS: 207012

SOFTWARE: RESECTED WINDOWNE Version 4.0
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPREBENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
154 ARSHWPIPHPCDTACPAPLPVVLVAPRSTILS--MSRTWTC----RRWAVAPCRAEKLMC 207
                                                                                                 68 VEPVCGDAAPACLLRTP----LRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQPW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 AAASATPMLSSKASLCIPTRGPPPQPLMRTPAARSHWPIPHPCDTACPAPLPVV----L 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            856 PSSSASP------HPCPSPLSNA-TAQSPLFILSPTVSPSPSPIPPVEPLMSA 901
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71,
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Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                    208 SSS 210
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US-09-949-016-11382
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US-09-949-016-11382
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Pactent No. 6551795

GENERAL INFORMATION:

PAPLICATION:

MUCHEIC ALINEOMATION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

PILE REPERRACE:

FILE REPERRACE:

FILE REPERRACE:

PRIOR PELICATION NUMBER: US 60/074,788

PRIOR PELING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18097

LENGTH: 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 A-AAGIA-----SSAVEPVCGDA-APACLLRTPLRGLL 89
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                 APPLICANT: TATOMATION.
APPLICANT: Vaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 1613-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR PILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 11.9%; Score 134.5; DB 2; Length 308; Best Local Similarity 29.0%; Pred. No. 0.00059; Matches 53; Conservative 18; Mismatches 83; Indels 29.
                                                                                                                                                                                                                                                                                                                                                                                                       ch 13.4%; Score 152; DB 2; Length 3118; Similarity 25.7%; Pred. No. 0.00025; 69; Conservative 27; Mismatches 92; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 ---PQPLMRTPAARSHWPIP--HPCDT-----ACPAPLPVVLVAPRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1558 PLPSPASTOTL -- ALAPALAPTLGGSS 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 -ILSMSRIWICRRWAVAPCRAEKLMCSS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 69, Conserv
    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
                                                                                                                                                                                                                                                                                       LENGTH: 3118
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                                                                                                                                                                                                                                                                                                               TYPE: PRT
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요 ò 셤 ò 셤 ઠે 쉽 ઠે

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999 PSSSASP------HPCPSPLSNA-TAOSPLPILSPTVSPSPSPIPPVRPLMSA 1044
                                                                                                                                                                                                                              942 TPDVC-PSSPA--LQTPSLSSGQLPPLLIPTDPSSPPPCPPVLTVATPPPPLLPTVPLPA 998
                                                                                                                                                                                                                                                                                       122 AAASATPMLSSKASLCIPTRGPPOPLMRTPAARSHWPIPHPCDTACPAPLPVV----L 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 942 TPDVC-PSSPA--LQTPSLSSGQLPPLLIPTDPSSPPPCPPVLTVATPPPPLLDTVPLPA 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 VEPVCGDAAPACLIRTP-----LRGLIKPTGPRSTMECPPALIVHPPAGGMASGSSQPW 121
                                                                                                                                                                                                 68 VEPVCGDAAPACLLRTP-----LRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQPW 121
                                                                                                               19 MGQRALPSSLALLSRPLSPP-----PAACSG-----DPGCGSGAGLPSASAAAGIASSA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  888 MLQKVLLNBYNGIDLPVENPADGTRSPSPCKSLBAQPDPDLGPGSGFPAPTV----ES
                                                                                                                                                     888 MIQKVLINEYNGIDLPVENPADGTRSPSPCKSLEAQPDPDLGPGSGFPAPTV----ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 MGQRALPSSLALLSRPLSPP-----PAACSG-----DPGCGSGAGLPSASAAAGIASSA
                                                                    45;
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                        Length 1719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4. Application US/08399411

Patent No. 5831008

GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastome Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITT: San Diego
STATE: California
COUNTRY: USA
                        Query Match
11.9%; Score 134.5; DB 1; Length 1
Best Local Similarity 28.3%; Pred. No. 0.0041;
Matches 54; Conservative 21; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1719 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.3%
Matches 54; Conservative
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US-08-399-411-4
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                                                                                                                                                                                                                                                                                                           19 MGQRALPSSLALLSRPLSPP-----PAACSG-----DPGCGSGAGLPSASAAGIASSA 67
                                                                                                                                                                                                                   Query Match
11.9%; Score 134.5; DB 2; Length 1540;
Best Local Similarity 28.3%; Pred. No. 0.0037;
Matches 54; Conservative 21; Mismatches 71; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08459568
Sequence 4. Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: USA
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 11383
LENGTH: 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
PILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPRENCE/DOCKET NUMBER: 9-LJ 1264
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: CHARATION FOR SEQ. ID NO: 4:
SEQUENCE CHARATICES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 VAPRSTILSMS 187
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US-08-459-568-4
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1045 ASPGPPTLSSS 1055
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US-09-586-472-4
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                122 AAASATPMLSSKASLCIPTRGPPOPLMRTPAARSHWPIPHPCDTACPAPLPVV-
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28.3%; Pred. No. 0.0041;
tive 21; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                           Sequence 4, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein
TITLE OF INVENTION: Zinc Finger Protein
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/399,411
FILING DATE: 06-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1719 amino acids
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Best Local Similarity 28.34
Matches 54; Conservative
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                                                                                              177 VAPRSTILSMS 187
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                                                    999 PSSSASP----
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STATE: California
COUNTRY: USA
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942 TPDVC-PSSPA--LQTPSLSSGQLPPLLIPTDPSSPPPCPPVLTVATPPPPLLPTVPLPA 998
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Sequence 4, Application US/09586472
; Patent No. 6123135
; GENERAL INFORMATION:
    APPLICANT: Huang, Shi
    TITLE OF INVENTION: Retinoblastoma Protein - Interacting
    NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.9%; Score 134.5; DB 2; Length 1
28.3%; Pred. No. 0.0041;
tive 21; Mismatches 71; Indels
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores Lip
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
PILING DATE: 01-Jun-2000
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 18-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1719 amino acids
                                                                                                                                                                                                                                                                                                                                             ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: (619) 535-900.
(619) 535-8949
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Best Local Similarity 28.3%
Matches 54; Conservative
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APPLICANT: Huang, Shi
APPLICANT: Chadwick, Robert B.
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                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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US-09-252-991A-28087
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                                                                                                                                                                                                                         LENGTH: 1719
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                                                                                                                                                                                                      SEQ ID NO 4
                                                                                                                                                                                                                                          TYPE: PRT
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                                                Sequence 4, Application US/09528706
Patent No. 6468985
GENERAL NO. 6468985
GENERAL SETTING MATION:
TITLE OF INVENTION: Retinoblastoma Protein - Interacting TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                ADDRESSEE: Campbell & Plores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 134.5; DB 2;
28.3%; Pred. No. 0.0041;
tive 21; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUWBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INPORMATION:
TELEPHONE: (619) 535-9001
TELEPRX: (619) 535-8949
INFORMATION FOR 'SEQ ID NO: 4:
SEQUENCE CHARACTERISITICS:
LENGTH: 1719 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 28.38
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Sequence 4, Application US/10024450 Patent No. 6927030

US-10-024-450-4

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS. AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            942 TPDVC-PSSPA--LQTPSLSSGQLPPLLIPTDPSSPPPCPPVLTVATPPPPLLPTVPLPA 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 AAASATPMLSSKASLCIPTRGPPQPLMRTPAARSHWPIPHPCDTACPAPLPVV----L 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 TRRGTPSWMSACANSSSASPGTC----ATRLAMRRRTSKNVACGSTASCSTTPSKASL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              888 MIQKVILNEYNGIDLPVENPADGTRSPSPCKSLEAQPDPDLGPGSGPPAPTV----ES 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 VEPVCGDAAPACLLRTP-----LRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQPW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 ---GLPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTWEC--PPALIVH 107
TITLE OF INVENTION: Methods of Detecting and Treating
TITLE OF INVENTION: Microsatellite-Instability Positive Tumors Using RIZ
FILE REPRENCE: P-LJ 5101
CURRENT APPLICATION NUMBER: US/10/024,450
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/256,582
NUMBER OF SEQ ID NOS: 15
SOFTHAMBE: FREEESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 MGQRALPSSLALLSRPLSPP-----PAACSG-----DPGCGSGAGLPSASAAGIASSA
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28.3%; Pred. No. 0.0041;
.ive 21; Mismatches 71; Indels
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11.8%; Score 133.5; DB 2;
Best Local Similarity 27.6%; Pred. No. 0.0008;
Matches 66; Conservative 14; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 28087, Application US/09252991A
; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 SPPQPRHPIQPSLPGTTSGS-LSSVPGAPAPAASKAPV----VPSPVLQSPSEGLGMGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 GP----ACP----LPPLAGGEAFPFPSPEQGLALSGAGFP-GMLGALPLPLSLGQPPPSP 260
PP----AGGMASGSSQPWAAAS-----ATPMLS----SKASLC----IPTRGPPPQP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
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                                                                       148 LMRTPAARSHWPIP-----HPCDTACPAPLPVVLVAPRSTILSMSRTWTCRRWAVA 198
                                                                                                         ---RCCRAWRC-RWAIA 317
                     -LSPPPAACSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%; Score 127; DB 2; Length 246; 24.9%; Pred. No. 0.002; ive 17; Mismatches 60; Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPRSTMECPPALIVHPPAGGMA-----SGSSQPWAAASATPM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.3%; Score 128; DB 2; Length 71
Best Local Similarity 27.5%; Pred. No. 0.0055;
Matches 64; Conservative 22; Mismatches 73; Indels
                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT PILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
SRIOR APPLICATION NUMBER:
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3402
LENGTH: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-104-047-2232

Sequence 2232, Application US/10104047

Patent No. 6942341

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: No. 6943241e1 full length cDNA

TITLE OF INVENTION: No. 6943241e1 full length cDNA

TITLE NEFFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: 2002-03-25

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

PRIOR FILING DATE:

NUMBER OF SEQ 1D NOS: 4096

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 QAAAPVDQTPRTLATMGQRALPSSLALLSRP.
                                                                                                           276 TSNGAKRASTWPSPTIRRIGVKATCSTGC-
                                                                                                                                                                                                    Sequence 3402, Application US/10104047
Patent No. 6943241
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11.2%
Best Local Similarity 24.9%
Matches 68; Conservative
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; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-3402
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US-10-104-047-3402
108
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Gaps

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----- ASATPMLSSKASLC----- 137
                                                                                                                                                                                                                                          104 LLPPCG---LCFSLPWSSLDLPELCOVGPGRPFPGPAVALSFLTCFHSCCPRWALGFVLL 160
                                                                                                                                                                                                                                                                                             ----GPPPOPLMRTPAARSHWPIPH 162
                                                                                                                                                                                                                                                                                                                                | | : :
| I | IKPFVLNLRGSRDWGIPSKELWLGAQKEGHRVLVGCPGSGPPPLPPPSLPASISVQGSPG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 LLPPCG----LCFSLPWSSLDLPELCQVGPGRPFPGPAVALSFLTCFHSCCPRWALGFVLL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 LKPFVLNLRGSRDWGIPSKELWLGAQKEGHRVLVGCPGSGPPPLPPPSLPASISVQGSPG 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
7 APVDOTPRILAT-----MGQR-ALPSSLA-LLSRPLSPPPAACSGDPGCGSGAGLPSASA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 APVDQTPRTLAT-----MGQR-ALPSSLA-LLSRPLSPPPAACSGDPGCGSGAGLPSASA
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                                             5 ASVDCTPPSLQTELLPPWGPRSSLPADCAPCLGTALLPPWGPCSSLPPCGPRSSLP
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                                                                                                60 AAGIASSAVEPVCGDAAPACLIRTPLRGLLKPTGPRSTM---ECPPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INCOGRAMION:
GENERAL INCORMATION:
APPLICANT: HELLX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length CDNA
TITLE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE:
PRIOR RPLICATION UNBER:
NUMBER: OF SEQ ID NOS: 4096
SOFTWARE: PRECENTIN Ver. 2.1
SEQ ID NO 2243
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                                                                                                                                                                                                                                                                                                                                                                                             PCDTACPAPLPVVLVAPRSTILSMSRTWTCRRW 195
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                                                                                                                                                                                              106 VHPPAGGMASGSSQPWAA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-104-047-2243
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Best Local Similarity
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US-10-104-047-2243
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Sequence

Sequence 38000, A Sequence 2, Appli Sequence 4, Appli Sequence 1, Appli Sequence 162087, Sequence 11887, A Sequence 38471, A Sequence 18031, A Sequence 18031, A Sequence 296496, Sequence 296496, Sequence 20553, A Sequence 20553,

US-10-425-115-262328 US-10-425-115-198645 US-09-8647-61-38000 US-10-142-650-1 US-10-024-450-4 US-10-0142-650-1 US-11-077-465-4 US-10-437-963-162087 US-10-425-115-315380 US-10-457-115-315380 US-10-457-115-315380 US-10-457-115-315380 US-10-437-963-162013 US-10-437-963-162013 US-10-437-963-118377 US-10-437-963-162013 US-10-437-963-118377 US-10-437-963-11837

ALIGNMENTS

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   238, App
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11_FUBCOMB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-440-76-8

US-10-440-73-93-8849

US-10-732-93-8849

US-10-732-93-8849

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence 238, Application US/09989890
; Sequence 238, Application WS/09989890
; Publication No. US20040166105A1
; GENERAL INFORMATION:
    APPLICANT: Salceda, Susana
; APPLICANT: Recipon, Herve
APPLICANT: Bluta, Jason
; APPLICANT: Bluta, Jason
; APPLICANT: Liu, Chenghua
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr.
    TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and P.
    TITLE OF INVENTION: UNMBER: US/09/989,890
    CURRENT APPLICATION NUMBER: US/09/989,890
    CURRENT FILING DATE: 2001-11-22
    NUMBER OF SEQ ID NOS: 280
    SOFTWARE: Patentin version 3.1
    SOFTWARE: Patentin version 3.1
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100.0%; Pred. No. 6.7e-73;
ive 0; Mismatches 0;
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US-09-989-920-206
'Sequence 206, Application US/09989920
'Patent No. US20020172957A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 212, Conservative
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ORGANISM: Homo sapien
US-09-989-890-238
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1897, Ap
149276,
168762,
116012,
60509, A
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72, Appl
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487 12971 1828 442 442 454 166 1008 569 883 413 842 842

Sequence Sequence Sequence Sequence

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138 136.5 136.5 135.5 135.5 135.5 135.1

Sequence

Sequence

US-10-767-701-34009

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61 AGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMA-SGSSQ 119
                                 61 AGIASSAVEAVCGDAAPACLLRTPLRGLKPTGPRSTMECPPALIVHPPTGGMARRAASQ 120
                                                                                   120 PWAAASATPMLSSKASLCIPTRGPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAP 179
                                                                                                           61 AGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMA-SGSSQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reita, Kalpan,
APPLICANT: Reita, Kalpan,
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific
TITLE OF INVENTION: Genes and Proteins
FILE REPERRACE: DEX-0313
CURRENT APPLICATION NUMBER: US/10/074,475
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR PILING DATE: 2002-02-13
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 295
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Pred. No. 5e-68;
1; Mismatches 8; Indels 1;
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                        Sequence 201, Application US/10074475; Publication No. US20030092898A1; GENERAL INFORMATION:
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Best Local Similarity 95.3%;
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
APPLICANT: Cafferkey, Robert
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US-10-074-475-261
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US-10-437-963-137918
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LENGTH: 218
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Sequence 251, Application US/0998920

Patent No. US20020172557A1

GENERAL INFORMATION:

APPLICANT: Recipon, Herve

APPLICANT: Chen, Yongming

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot

FILE REFERENCE: DEX-0291

CURRENT APPLICATION NUMBER: US/09/989,920

CURRENT FILING DATE: 2001-11-21

PRIOR PILIANG DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 284

SOFTWARE: Patentin version 3.1

LENGTH: 213
               APPLICANT: Macina, Roberto
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
CURRENT ENVERNION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR PILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SEQ ID NO 206
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMA-SGSSQ 119
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Pred. No. 2.5e-68;
1; Mismatches 8;
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Best Local Similarity 95.3%;
Matches 203; Conservative 1
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Best Local Similarity 95.3'
Matches 203; Conservative
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j ORGANISM: Homo sapien
US-09-989-920-251
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapien
      GENERAL INFORMATION:
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US-09-989-920-251
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1018 PAPASAPLTIPISAPLTVSASG----PALLTSVTPPLAPVVPAAPGPPSLAPSGASPSAS 1073
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                                                                                                                                                                                                                                                                                           221 SPMSPSAPMPSTPST--TRAPRATRASTTL---PLPGPPPRAMRPAPAPAPAAAAPMP 275
                                                                                                                                                                                                                                                                                                                                                                                         276 RSTAAATSPLTWISPLTSPLTWISPRISIPRISSPSSTATTPPAAPTPRILILAV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                          107 HPPAGGMASGS----SQPWAAAS------ATPMLSSK---ASLCIP----- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 AAAPATMTSTAPLPEPWPWLAASTPPPPIPALRLTLAATPATRSRSTTAPAAVPGVTAAS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 --TRGPP----------PQPLMR----TPAARS-HWPIPHPCDTACPA-- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 SSTTTPPLLTTMPVALLTAPPSATRSIPLPLSRPTTATPÄTRSIPLPSPKPRPTÄTPÄAR 455
                                                                                                                                                                                                                                                                                                                                         56 SASAAAGIASSAVEPVCGDAAPACLIRT-PIRGILKPTGPRSTMECPPA-----LIV
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                                                                                                                                                                                                                                               1 SPHQAAAPVDQTPRTLATMGQRALPSSLALLSRPL-SPPPAAC----SGDPGCGSGAGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 KPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPP----
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhang, Bing
APPLICANT: Cland, Bradford W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Glbson, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: VARIANT
; LOCATION: 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-408-765A-2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.6%; Score 154; DB 4; Length 1480; Best Local Similarity 25.7%; Pred. No. 0.017; Matches 69; Conservative 27; Mismatches 92; Indels 8
                                                                                                                                                                   Pred. No. 0.0034;
); Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 ----PLPVVLVAP-----RSTILSMSR 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 STSTPLPLPAPAPPWLMTRARLLMTAR 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2239, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S. APPLICANT: Pahy, Boin D.
                                                                                                                                              29.0%; Pic. 20;
                                                                                                                                                                   Best Local Similarity 29.03
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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Sequence 137896, Application US/10437963

Publication No. US20040123343A1

Sequence 137896, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION UMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 137896

LEMIGTH: 487
us-09-989-89

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 137918

LENGTH: 556

TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 PAPXPLGPAQPHXTPRAAPKPPPWPPPRTAALPSSSPRSPCPLSSRRPPRRGAAPTXPTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 -----CLLRTPLRGLLKPTGPRSTMECPPAL------IVHPPAGGMASGSSQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 25.8%; Pred. No. 0.0019;
Matches 71; Conservative 15; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: PAT_MRT4530_39355C.1.pep
US-10-437-963-137918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_39335C.1.pep
US-10-437-963-137896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              450 LPSP-----RSSWRRWPCPRSSRRPRA 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(556)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Oryza sativa
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90 KPTGPRSTMECPPALIVHP-PAGGMASGSSQ---PWAAASATPMLSSKASLCIPTRGPPP 145
            Query Match 13.4%; Score 152; DB 5; Length 2971; Best Local Similarity 25.7%; Pred. No. 0.045; Matches 69; Conservative 27; Mismatches 92; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LAL, Preet,
APPLICANT: LAL, Preet,
APPLICANT: LAL, Dyung Aina M.
APPLICANT: PATTERSON, Chandra
APPLICANT: AZIMZAI, Yalda
APPLICANT: BANDMAN, Olga
APPLICANT: TANG, Y. Tom
APPLICANT: BANDMAN, Olga
APPLICANT: BARH, Purvi
APPLICANT: BIRH, Purvi
APPLICANT: REDDY, Roopa
TITLE OF INVERTION: TRANSCRIPTION FACTORS
FILE REFERENCE: PF-0761 PCT
CURRENT APPLICATION NUMBER: US/10/221, 625
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                  183 -ILSMSRTWTCRRWAVAPCRAEKLMCSS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 15, Application US/10221625; Publication No. US20040033942A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: VIB, Henry
APPLICANT: LAL, Preeti
APPLICANT: LU, Preeti
APPLICANT: BATTERSON, Chandra
APPLICANT: PATHERSON, Chandra
                                                                                                                                                                        59 A-AAGIA------
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Matches 65, Conservative
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US-10-221-625-15
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US-10-732-923-8849

US-10-732-923-8849

Sequence 8849, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

APPLICANT: Edgerton, Michael D

TILLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

FILE REFERENCE: 38-15 (52796)C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2002-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 13.4%; Score 152; DB 4; Length 2971; Similarity 25.7%; Pred. No. 0.045; 69; Conservative 27; Mismatches 92; Indels 8
                                                                                                                                                                                                  APPLICANT: Scuttain, inclusion
APPLICANT: Gout, Ivan
APPLICANT: Gout, Ivan
APPLICANT: Goute, Ali
APPLICANT: Gure, Ali
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd
TITLE REPRENCE: LO0461/70130(JRV)
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US 60/291,150
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 82
SEQ ID NO 50
LENGTH: 2971
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                                                                                                                              Sequence 50, Application US/10146473 Publication No. US20030108888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-AAGIA-----
                                                                                                                                                                                    APPLICANT: Scanlan, Matthew
APPLICANT: Gout, Ivan
APPLICANT: Stockert, Elisak
APPLICANT: Gure, Ali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 8849
LENGTH: 2971
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; ORGANISM: Homo sapiens
US-10-732-923-8849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-50
                                                                                              RESULT 8
US-10-146-473-50
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Best Local S:
Matches 69
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                                                                            1245 ALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVAPACSPVLVPASALASPFPSAP 1304
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                                               28
                                                                                                                                          ------SSAVEPVCGDA-APACLLRTPLRGLL 89
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                                            2 PHOAAAPVD---QTPRTLATMGQRALPSSLALLSRPLSPPAACSGDPGCGSGAGLPSAS
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                                                                                                                                                                                                                                                                                                                                       145 --- POPLMRIPAARSHWPIP--HPCDI-----ACPAPLPVVLVAPRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040033942A1 879500CD1
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Page 5

APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cac, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 102727
LEBNOTH: 454
TYPF.
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 149274
LENGTH: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS-PTTSSPPTPVARSPMTPSVPXDLPAPPTRPRGPPPHRMASPLPRSTPPALIPASPPP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 PPPAACSGDPG-----GGSGAGLPSASAAAGIASSAVEPVC----GDAAPACLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 GORSPIPRAHSPDPPPLRAGHRRXPQPLPRAADPALPKAAPPNPPXPIPSPPPPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.7%; Score 144.5; DB 4; Length 454; 28.4%; Pred. No. 0.025; Live 16; Mismatches 69; Indels 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_100222C.1.pep
US-10-437-963-102727
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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ORGANISM: Oryza Bativa
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Barbazuk, Brad Applicant: Barbazuk, Brad Applicant: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement PILE REPERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                    146 OPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAPRSTILSMSRTWTCRRWAVAPCRAEKL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 RPSLTGVASPRPSPPAAPXSSPSPPPPPIEYAAAGCACFLSHIARCFHLPPPRAPRRG- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 LKPTGPRSTMECPPALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGP---- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 PSPPSPVAVRALPPAAALAPPP---IPSASQPRACHPRXPRSVPHPSRTLPPTAPXSKTP 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 PHPNPPPPLTHTHTAAPQVAPPPAHSPAASPPPPPPPPPSRALPCPYPLLFSSSYPPIFS 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ----GAGLPSASAAAGIASSAVEP-----VCGDAAPACLL------RTPLRGL 88
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13.0%; Score 147.5; DB 4; Length
Best Local Similarity 26.6%; Pred. No. 0.015;
Matches 65; Conservative 14; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_93584C.1.pep
US-10-437-963-197867
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 197867, Application US/10437963
Sequence 197867, Application US/10437963
SEGNERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
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                                                                                                                                                                                                                                                                       251 TPVL----
                                                                                                                                                                                                                                                                                                                     206 MCSS 209
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US-10-437-963-102727
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Search completed: March 16, 2006, 16:00:53
Job time : 166 secs
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ORGANISM: Oryza sativa
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Best Local Similarity
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                                                                                                                                                                                81 SPXPPPPEXPAPPRPLPPSSLPPPPAPSSTITTTTATPPPXPSAPLADPPAPLPPPPSSXP 140
                                                                                                                                                                                                                         47 GCGSGAGLPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIV 106
                                                                                                                                                                                                                                                       141 SSPSPPPAPSPPAPSSPSAPSP----PPAPSSPPXPP----SPPHPRPTKQMPP---- 188
                                                                                                                                                                                                                                                                                           107 HPPAGGMAS---GSSQPWAAASATPMLSSKASLCIPT----RGPPPQPLMR----- 150
                                                                                                                                                                                                                                                                                                                189 -PPASSRRSTPRSXSPPWPASPSPHSSSSPSAASSTARPIRRPPPTPTVKPTSSTMVV 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 TGPRSTMECPP--ALIVHPPAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPPQPLM 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 R-----TPAARSHWPIPHPCDTACPAPLPVVLVAPRSTILSMSR---TWTCRRWAV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 RRPPALPPPLPPAARGAPPRP-PAARGAPPPPP---VAP-STFVSAGRGRMRWRLTCGGS 160
                                                                                                                                                         46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 SRPLSPPPAACSGDPGCGSGAGLPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKP 91
                                                                                                                                                       1 SPHQAAAPVDQTPRTL--ATMGQRALPSSLALL----SRPLSPPPAAC---SGDP
                                                                                                                       Gaps
                                                                                                                       51;
                                                                                     Length 373;
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                                                                                                                       Indels
                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_49623C.1.pep
US-10-437-963-149274
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                                                                                   12.7%; Score 143.5; DB 4; 29.2%; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                            151 TPAAR----SHWPIPHPCDTACPAPLPVVLVAP 179
                                                                                                                                                                                                                                                                                                                                                                                    || || || || TPPARPSPRPTSTPPPPAGLP-PLPLPLPLP 282
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                     63; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
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Publication No. US20040123343A1
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                                                                                                   Local Similarity
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                                                                                   Query Match
Best Local
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Go, Yongwei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 10431/963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 190430
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OTHER INFORMATION: unsure at all Xaa locations
Sequence 190430, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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310 PAPTPPLLPHPGTPLPTLT 328
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Sequence 2233, Ap
Sequence 2247, Ap
Sequence 4927, Ap
Sequence 4926, Ap
Sequence 31, Appl
Sequence 23509, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31, Appl
23509, A
2246, Ap
20771, A
1, Appli
26110, A
23618, A
2, Appli
6, Appli
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89, Appl
24535, A
2501, Ap
                                                                 March 16, 2006, 15:58:16 ; Search time 23 Seconds (without alignments) 263.828 Million cell updates/sec
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                                                                                                                                           212
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-096-568A-4926
US-11-096-568A-23509
US-11-096-568A-23509
US-11-096-568A-2071
US-11-096-568A-26110
US-11-096-568A-26110
US-11-096-568A-26110
US-11-096-568A-26110
US-10-06-568A-26110
US-10-06-568A-26110
US-10-06-568A-26110
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US-11-036-256-89
US-11-096-568A-24535
US-11-096-568A-2501
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US-10-967-648A-14
US-10-330-773-668
                                                                                                                                                                                                                           of hits satisfying chosen parameters:
                                                                                                                                                                                                   169630 segs, 28622889 residues
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Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
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seq length: 200000000
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Maximum DB
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Sequence 1871, Ap
Sequence 27199, A
Sequence 10, Appl
Sequence 24112, A
                                            661, App
12515, A
25807, A
25807, A
26807, A
11657, A
20128, A
20113, A
20211, A
20211, A
20211, A
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Sequence
Sequence
US-10-330-773-663
US-11-096-568A-2263
US-11-096-568A-12515
US-11-096-568A-25806
US-11-096-568A-25807
US-11-096-568A-25807
US-11-096-568A-25807
US-11-096-568A-24229
US-11-096-568A-2012
US-11-096-568A-2012
US-11-096-568A-2011
US-11-096-568A-2011
US-11-096-568A-2011
US-11-096-568A-1897
US-11-096-568A-1897
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ALIGNMENTS

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APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: KIELISZEWSKI, MARCIA
TITLE OF INVENTION: WETHODS OF PRODUCING PREPTIDES/PROTEINS IN PLANTS AND
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
TITLE OF INVENTION: WOMBER: US/11/036,256
CURRENT APPLICATION NUMBER: 06/602,562
PRIOR PELING DATE: 2004-00-13
PRIOR PELING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: 60/532,027
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR APPLICATION NUMBER: 60/536,486
PRIOR PELING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 33
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 PHSPPPDLSPSPTPTPPLGPHSPPPTLSPSPTPTPPPGPHSPPPPLSPSPTPTPPLGPHS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPAL----IVHPPA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGMASGSSQPWAA - - ASATPMLSSKASLCIPTRGPPQPLMRTPAARSHWPIPHPCDTAC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPVSGTPLPTLTPLPAPTPPLLPHPGTPLPTLTPLPAP---TPPLLPHPGTPLPTLTPL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 PPFILS---PSPTPPPGPHSPPG----PPLSPSPTPPLGPHSPPFTLSPSPTPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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11.3%; Score 128.5; DB 7; Length 346;
Best Local Similarity 26.6%; Pred. No. 0.0047;
Matches 53; Conservative 19; Mismatches 104; Indels 23
Sequence 33, Application US/11036256 Publication No. US20060026719A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPLPVVLVAPRSTILSMS 187
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US-11-072-512-2243
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LENGTH: 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 D------PGCGSGAGLPSASAAAGIASSAVEPVCGDAAPACLLRTPLRGLLKPT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 LSSKASLCIPTRG---PPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLVAP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.3%; Score 128; DB 7; Length 710; Best Local Similarity 27.5%; Pred. No. 0.01; Matches 64; Conservative 22; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NASUHIXO
TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 QAAAPVDQTPRTLATMGQRALPSSLALLSRP--
Sequence 3402, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISCGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
                                                          SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                               TAMECHIKA, ICHIRO
SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
                                                                                                                                                                        HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-11-072-512-3402
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APPLICANT:
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Sequence 2232, Application US/11072512;
Publication No. US20060029945A1;
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO;
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: WAKAMATSU, APPLICANT:
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO

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61 ------GDRAPPS-LRTALG---PPWGPRPSLPADRAPPSLGTSLPPPSLRTV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GPPPQPLMRTPAARSHWPIPH 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 APVDQTPRTLAT-----MGQR-ALPSSLA-LLSRPLSPPPAACSGDPGCGSGAGLPSASA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ASVDCTPPSLQTELLPPWGPRSSLPADCAPCLGTALLPPWGPCSSLPPCGPRSSLP---
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Best Local Similarity 24.9%; Pred. No. 0.0045;
Matches 68; Conservative 17; Mismatches 60; Indels 128; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAGAHERI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OP INVENTION: NOVEL full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2002-01-105
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN VEY: 2.1
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Publication No. US20060029945A1
GENERAL INPORMATION:
APPLICANT: ISCOAI, TAKAO
APPLICANT: O'TSIKI, TETSUJI
APPLICANT: O'TSIKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISAIO, HIROYUKI
APPLICANT: ISAIO, YUNO
APPLICANT: ISONO, YUNO
APPLICANT: HOO, YUNI
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                                                                                                                              IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                            OTSUKA, KAORU
NAGAI, KEIICHI
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US-11-072-512-2232
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APPLICANT:
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Sequence 4926, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE REFERENCE: 2750-1592PUS2
CURRENT PALLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4926
                                                                                                                                                     63 IASS--AVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPAL--IVHPPAGGMASGS- 117
                                                           77 PASSPTVASPPSKAAAPAPVATPPAATPPAAT----PPAVTPVSSPPAPVPVSSPP 133
                                                                                                                   118 ----SOPWAAASATPMLSSKASLCIPTRGPPPQPLMRTPAARSHW-PIPHPCDTACPAP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 IASS--AVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPAL--IVHPPAGGMASGS- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 PASSPTVASPPSKAAAPAPVATPPAATPPAATPPAAT----PPAVTPVSSPPAPVPVSSPP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 ----SOPWAAASATPMLSSKASLCIPTRGPPQPLMRTPAARSHW-PIPHPCDTACPAP 171
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Publication No. U320060026719A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIELISZEWSKI, MARCIA
APPLICANT: XU, JIANFENG
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
FILE REPERRUCE: 27211/04130
CURRENT APPLICATION NUMBER: US/11/036,256
CURRENT FILING DATE: 2006-01.14
PRIOR PILING DATE: 2006-01.8
PRIOR PILING DATE: 2004-06-22
PRIOR FILING DATE: 2004-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 125.5; DB 7; Length 2; Pred. No. 0.0058; 16; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1).7(246)
; OTHER INFORMATION: Ceres Seq. ID no. 14305844
US-11-096-568A-4926
                                                                                                                                                                                                                            172 LPVVLVAPRSTILSMS 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 -PV--GAPGSSQDSMS 210
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Best Local Similarity 33.2%;
Matches 65; Conservative 10
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ORGANISM: Glycine max
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US-11-096-568A-4926
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Publication No. US20060048240A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 4927
LENGTH: 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 ASVDCTPPSLQTELLPPWGPRSSLPADCAPCLGTALLPPWGPCSSLPPCGPRSSLP---- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 APVDQTPRTLAT-----MGQR-ALPSSLA-LLSRPLSPPPAACSGDPGCGSGAGLPSASA 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 128; Gaps
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11.2%; Score 127; DB 7; Length 246;
Best Local Similarity 24.9%; Pred. No. 0.0045;
Matches 68; Conservative 17; Mismatches 60; Indels 1
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33.2%; Pred. No. 0.0057;
ive 16; Mismatches 86;
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NAME/KEY: misc_feature
LOCATION: (1)...(240)
OTHER INFORMATION: Ceres Seq. ID no. 14305845
APPLICANT: NAGABARI, KENJI
APPLICANT: NAGABARI, KENJI
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 08433-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR PILING DATE: 2005-03-07
PRIOR PILING DATE: 2002-01-25
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENT OF SEQ ID NOS: 4096
SOFTWARE: PATENT VET: 2.1
SEQ ID NO 2243
LENGTH: 246
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Matches 65; Conservative
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US-11-072-512-2243
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ORGANISM: Glycine max
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Sequence 20771, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION: GEOGRAPHICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 LSSAGPPPVLPPPSLFSAGPPPVLPPP---SLSSTAPPPVMPLPPLSSATPPPGTPPPGV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.8%; Score 123; DB 7; Length 723; Best Local Similarity 29.8%; Pred. No. 0.024; Matches 48; Conservative 12; Mismatches 81; Indels
201 ADTVPVVAPTVAAATAPRSPTPQRPRRGTLPPTAPRRRLSQRQRT 245
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TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
                                                                                                                                                                      Sequence 2246, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 PVDQTPRTLATMGQRALPSSL
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SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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NAGAI, KEIJICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                                                                                                                                 APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4096
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US-11-072-512-2246
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APPLICANT:
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Subblication No. U320060048240Al
SUBNERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: DATE: US. 11,096,568A
CURRENT APPLICATION NUMBER: US./11/096,568A
NUMBER OF SEQ ID NOS: 34471
SEQ ID NOS: 34471
SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PHSPPPLSPSPTPTPPLGPHSPPPTLSPSPTP-TPPPGPHSPPPLS-----PSPTPT- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GIASSAVEPVCGDAAPACLIRTPIRGLIXPTGPRSTMECPPALIVHP-PAGGMASGSSQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 -----PPLGPHSPPPTL-SPSPTPTPPGPHSP----PPPLSPSPTPTPPLGPHSPPD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 WAAASATPMLSSKASLC---IPTRGPPPQPLMRTPAARSHWPIPHPCDTACPAPLPVVLV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 TLSPSPTPTPPPGVPVSGTPLPTLTPLPAP---TPPLLPHPGTPLPTTPLPAPTPPLLP 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 SSAVEPVCGDAAPACILRTPLRGLLKPTGPR----STMECPPALIVHPPAGGMASGSSQP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 WAA-----ASATPMLSSKASLC-IPTRGPPPOPLMR----TPAARSHWPIPHPCDTACPA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 RAAPTAASTSASPSRSRPGTTTPTPTRPRPTPTRAAAPVTPTAR---PLLLPAATTAPE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAAGIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 ATATSSPTPWCGSTPAASARPASTSTTAR-----ARRGTRSCSSRSRPPPASTTPSST 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPPAACSGDPGCGSGAGLPSASAAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.8%; Score 123; DB 7; Length 355; Best Local Similarity 27.6%; Pred. No. 0.013; Matches 62; Conservative 20; Mismatches 101; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: amino acid construct
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.8%; Score 123; DB 7; Length 228;
Best Local Similarity 27.8%; Pred. No. 0.0084;
Matches 52; Conservative 17; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 PLPVVLVAPRSTILSMSRTWT---CRRWAVAPCRAEKLMCSSSRS 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(355)
; OTHER INFORMATION: Ceres Seq. ID no. 12413224
US-11-096-568A-23509
   PRIOR APPLICATION NUMBER: 60/536,486
PRIOR FILING DATE: 2004-01-14
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 31
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
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222 HPGRTMV 228
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US-11-096-568A-23509
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Sequence 26110, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: 1592PUS2
CURRENT PELICATION UNDER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23618, Application US/11096568A
| Publication No. US20060048240A1
| GENERAL INFORMATION:
| APPLICANT: Alexandrov, Nickolai et al.
| TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
| TITLE OF INVENTION: Therby
| TITLE OF INVENTION: Therby
| FILE REFERENCE: 2750-1592PUS2
| CURRENT APPLICATION NUMBER: US/11/096,568A
| CURRENT FILING DATE: 2005-04-01
| NUMBER OF SEQ ID NOS: 34471
| SEQ ID NO 23618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 LKPTGPRSTMECPPALIVHPPAGGMASGSS--QPWAAASATPMLSSKASLCIPTRGPPPQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 ----SSASASGCSSASPSAPPSCSCSSSSSSASPAAAAA-----ASPPTPTTPPTPS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 PLARTPAARSHWPIPHPCDTACPAPLPVVLVAPRSTILSMSRTWTCRRWAVAPCRAEKLM 206
701 PQERSQQPLSAEG--PHLSVPASVIVSAPPPAQDPAPATPVAKGAGLGPQAPDSQASPAP 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 LSRPLSPPPAACSGDPGCGSGAGLPSASAA--AGIASSAVEPVCGDAAPACLLRTPLRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.6%; Score 120; DB 7; Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 120; DB 7; Length 242
Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1).7(242)
; OTHER INFORMATION: Ceres Seq. ID no. 13498595
US-11-096-568A-26110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no. 12414168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.6%;
Matches 55; Conservative 1
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ORGANISM: Zea mays subsp.
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                                               172 LPVVLVA 178
                                                                                          759 APQIPAA 765
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                                                                                                                                                                   RESULT 12
US-11-096-568A-26110
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US-11-096-568A-23618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 26110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 SSSPPTSSRSSCSRSSPSPPCSPSPPS----TP-----PSATRSPSRACSPSCPASGG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 VHPPAGGMASGSSQPW-----AAASATPMLSSKAS-LCIPTRGPPPQ-PLMRTPAARS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 GSPPRSSPPSRSSSPTTPSPCSSSASSPRTTAPASRACSPSSPSPTCSASSTSASSG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 APHSGAHSAHILSAAPIQ-----VGQPALFQMPVSLAAGSLPTQSQPAPAG--PAAT 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 TVLQGVTLPPSAVAMLNTPDGLVQPATPAAATGRAAPVLTVQPAPQAPPAVSTPLPLGLQ 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 S---GAGL-PSASAAAGIASSAVEP-----VCGDAAPACLLR------TPL-RGLL 89
                                                                                                                                                                                                                                                                                                                -----SACSGDPGCG---S
                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yang, Bing
APPLICANT: Yang, Bing
APPLICANT: Wang, Liang
TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
TITLE OF INVENTION: 0799-565001
CURRENT APPLICATION NUMBER: US/11/059,982
CURRENT APPLICATION NUMBER: US 60/545,573
PRIOR FILING DATE: 2004-02-17
PRIOR FILING DATE: 2004-02-17
NUMBER OF SEQ ID NOS: 50
SOPTWARE: FRACESO for Windows Version 4.0
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                                                                                                                                                                                                                   Length 413;
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10.6%; Score 120.5; DB 7; Length
Best Local Similarity 26.3%; Pred. No. 0.077;
Matches 65; Conservative 17; Mismatches 84; Indels
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 HWPIPHPCDTACPAPLPVVLV-----APRSTILSMSRT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 TSPASSPCSRTTRASPPCARARTSSGGSSSPR--VLSSSRS 320
                                                                                                                                                                                                              Query Match 10.7%; Score 121.5; DB 7;
Best Local Similarity 25.3%; Pred. No. 0.019;
Matches 56; Conservative 24; Mismatches 80;
                                                                                                                                                                                                                                                                                                              1 SPHQAAAPVDQTPRTLATMGQRALPSSLALLSRPLSPPP-
                                                                                                              ; LOCATION: (1)...(413)
; OTHER INFORMATION: Ceres Seq. ID no. 12387083
US-11-096-568A-20771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/11059982
Publication No. US20050255507A1
GENERAL INFORMATION:
                                               mays
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                                             ORGANISM: Zea mays subsp.
                                                              FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jenkins,
APPLICANT: Yang, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-059-982-1
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Sequence 2, Application US/10467033

Publication No. US20060019248A1

GENERAL INFORMATION:

APPLICANT: Triziani, Valdenize

APPLICANT: Olsen, Yasuyoshi

APPLICANT: Olsen, Bjorn K.

TILLE OF INVENTION: Mitant SH3-Binding Protein Compositions and Methods

FILE REPERENCE: H0498.70204US00

CURRENT APPLICATION NUMBER: US/10/467,033

CURRENT FILING DATE: 2003-08-01

PRIOR PLING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 113

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 561
                                  12;
                                                                                                          156 AGTPGSPRPPTSAASSCRATRPAAPSRTTSPCASVARPRTWPPSPC-GDTSSSCHSSA-- 212
                                                                                                                                                   55 PSASAAAGIASSAVEPVCGDAAP----ACLIRTPIRGLIKPTGPRSTMECPPALIVHP 108
                                                                                                                                                                                       213 -- AWRARGRRPSA-PPILSSTGPSTTATGACRCRRAPR----PTTPWPTRSAPARRRWTP 265
                                                                                                                                                                                                                               109 PAGGMASGSSQPWAAASATPMLSSKASLCIPTRGPPPQP------LMRTPAARSHW 158
                                                                                                                                                                                                                                                      SSAVEPVCGDAAPACLLRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQPW--- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 DSKRDPLCPRRAEPC-PRVPATPRRMSDPPLSTMPTAPGLRKPPCFRESASPSPEPWTPG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ----AAASATPMLSSKASLC-----IPTRGPPPQPLMRTPAARSHWPIPHPCD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 PIPHPCDTACPAPLPVVLVAPRSTILSMSRTWTCRRWAVAPCRAEKLMC----SSSR 211
                                                                                                                                                                                                                                                                                                                                8 PVDQTPRTLATMGQRALPSSLALLSR---PLSPPPAACSGDPGCGSGAGLPSASAAGIA
                                                                        5 AAAPVDQTPRTLATMGQRA-----LPSSLALLSRPLSPPPAACSGD--PGCGSGAGL
                                  54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.6%; Score 120; DB 6; Length 561; Best Local Similarity 28.8%; Pred. No. 0.033; Matches 63; Conservative 16; Mismatches 100; Indels
              Pred. No. 0.022;
2; Mismatches 98; Indels
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63; Conservative
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ORGANISM: homo sapiens
              Best Local Similarity
Matches 63; Conserv
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US-10-467-033-2
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Sequence 6, Application US/10467033; Publication No. US20060019248A1; GENERAL INFORMATION:
APPLICANT: Tiziani, Valdenize; APPLICANT: Reichenberger, Ernest; APPLICANT: Olsen, Yasuyoshi
APPLICANT: Olsen, Bjorn R.

US-10-467-033-6

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65 SSAVEPVCGDAAPACILIRTPLRGLLKPTGPRSTMECPPALIVHPPAGGMASGSSQPW--- 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Mutant SH3-Binding Protein Compositions and Methods FILE REFERENCE: H0498.70204US00
CURRENT APPLICATION NUMBER: US/10/467,033
CURRENT FILING DATE: 2003-048-01
PRIOR APPLICATION NUMBER: US 60/266,129
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PVDQTPRTLATMGQRALPSSLALLSR---PLSPPPAACSGDPGCGSGAGLPSASAAGIA
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NAME/KRY: MISC FEATURE
LOCATION: (415)..(415)
OTHER INFORMATION: Xaa = any amino acid
OTHER INFORMATION: provided that the mutant domain is not wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (418)...(418)
OTHER INFORMATION: Xaa = any amino acid
OTHER INFORMATION: provided that the mutant domain is not wild type
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NAME/KEY: MISC FEATURE
LOCATION: (420)...(420)
OTHER INFORMATION: Xa = any amino acid
OTHER INFORMATION: provided that the mutant domain is not wild type
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10.6%; Score 120; DB 6; Length 561;
Best Local Similarity 28.8%; Pred. No. 0.033;
Matches 63; Conservative 16; Mismatches 100; Indels
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                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                           LENGTH: 561
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AX335029 Sequence
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BC079148 Rattus no
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AC0718963 Rattus no
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AC026998 Homo sapi
AP001754 Homo sapi
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109630 Sequence 4
AR621538 Sequence
AR611912 Sequence
CQB5808 Sequence
AK128822 Homo sapil
AL939119 Streptomy
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
                                     AK091952 Homo sapi
AL592304 Homo sapi
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
 Human DNA
                     Sequence
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PE Corporation (NY) (US)
Location/Qualifiers
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CQ717675
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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ACCESSION
VERSION
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SOURCE
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CQ717675
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                                     ORIGIN
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-DB-GenEmbl -OFMT=fastap -SUPFIX=pan.rge -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=100 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORES=pt -THR MAX=100 -TRR MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-NO UNAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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                 GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                           OM protein - nucleic search, using frame plus p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Parage, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, N.J., Peters, G.J., Ackernan, R.J., Malahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodrgren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevohenko, Y., Bouffard, G.G., Blakesley, R.W., Toucham, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnert, A., Schein, J.T.E., Jones, S.J. and Marra, M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 43 Row: c Column: 17.

Location/Qualifiers
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Direct Submission
Submitsed (25-070-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                    human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Tissue Procurement: ATCC
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1 (bases 1 to 1679)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Strausberg, R.L., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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        Length:
Matches:
Conservative:
Mismatches:
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                                                             Percent Similarity:
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Alignment Scores: 5.74e-26 Length: 1679 Pred. No.: 5134.00 Matches: 212 Score: 1134.00 Matches: 212 Bercent Similarity: 100.0\$ Conservative: 0 Best Local Similarity: 100.0\$ Mismatches: 0 Ouery Match: 8 Indels: 0 DB: 8 Gaps: 0	Oy 1 SerProHisGlnalaalaalaProValaspGlnThrProArgThrLeualaThrMetGly 20	Qy 21 GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProProProAla 40 Db 98 CAGAGAGCATTACCTTCATCTCGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCT 147	Qy 41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla 60 Db 148 GCCTGCTCTGGCGACCTGGGAGTGGTGCTGCCTGCCTTCTGCTTCGCCGCT 207	Qy 61 AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu 80 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 81 LeuArgThrProLeuArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCys 100 Db 268 CTGAGGACTCCACTGAGGGACTGCTGAAGCCAACGGCCAAGGAGCACAATGGACTGC 327	Qy 101 ProproAlaLeuIleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro 120 Db 328 CCCCCAGCCCTGATGGACCCCCCCAGCCGGGGATGGCCAGCGCTCAAGTCAACCA 387	Oy 121 TrpalaalaaseralaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr 140	Oy 141 ArgGlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle 160	Qy 161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg 180 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 181 SerThrIleLeuSerMetSerArgThrTrpThrCysArgArgTrpAlaValAlaProCys 200 D 568 AGTACTATTCCATGAGTCGGACCTGGAGAGATGGGCAGTGGCTCCATGT 627	Oy 201 ArgalaGluLysLeuMetCysSerSerArgSer 212 	AX644347 LOCUS AX644347 LOCUS AX644347 DBFINITION Sequence 105 from Patent W002077232.	VERSION AX644347.1 GI:28610406 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;	REFERENCE 1 AUTHORS Salceda,S., Macina,R.A., Recipon,H., Pluta,J., Sun,Y. and Liu,C. TITLE Compositions and methods relating to breast specific genes and JOURNAL Prent: WO 02077232-A 105 03-OCT-2002; Diadexus, Inc. (US) FEATURES Location/Qualifiers

SOURCE

COMMENT

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/locus tag="RP11-344H11.4-001"
/note="match: Torcteins: Sw:P23358 Sw:P30050 Sw:P35979
Tr:AAM68299 Tr:CAA16156 Tr:EAA13367 Tr:O60886 Tr:Q7ZUG1
Tr:O86ZX1 Tr:O8AVWO Tr:Q8CZKO Tr:Q90XV6 Tr:Q9NQ02"
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Tr:BAA12661 Tr:Q7ZWJ3 Tr:Q8TBUI Tr:Q9CPZZ Tr:Q9NRPO
Tr:Q9PO75 Tr:Q9TR4"
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14033, .84877
gene="RP11-344H11.3"
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29398 .29403
//gene="RP11-344H11.8"
//locus_tag="RP11-344H11.8-001"
29419
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/db_xref="PSEUDO:CAI13556.1"
complement (50415. .50811)
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/pseudo
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                                                                                                                                                                                                                                                                                                        Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk cn Jun 17, 2002 this sequence version replaced gi:20218554.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group.

Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RP11-344H11 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Location/Qualifiers

1. .140207

/organism="Homo sapiens"
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Em:BC0127790.2 Em:BC014160.1 Em:BC014160.2 Em:BC038001.1"
join[21772. 22032.27482. .28495)
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="Sequence from overlapping clone RP4-633N17
(AL137860). Assembly confirmed by restriction digest."
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join(21468. _22032,27482. .28803,29251. .29417)

/gene="RP11-344H11.8"

/locus_tag="RP11-344H11.8-002"

join(21468. _22032,27482. .28803,29251. .29417)

/gene="RP11-344H11.8"
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oin(21603. .22032,27482. .29419)
gene="RP11-344H11.8"
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|gene="RP11-344H11.8"
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product="novel protein"
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Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
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/db_xref="taxon:9606"
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/clone_lib="RPCI-11.2"
496. .726
                                                                                                                                                 Hominidae, Homo.
1 (bases 1 to 140207)
sapiens (human)
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                                             Homo sapiens
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AUTHORS
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                               181 SerThrileLeuSerMetSerArgThrTrpThrCysArgArgTrpAlaValAlaProCys
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                                                                                                   161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg
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                                                                                121 TrpAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr
                                                                                                                                            141 ArgGlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle
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Patent: EP 1308459-A 799 07-MAY-2003;
Hellx Research Institute (JP) ; Research Association
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Mismatches:
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Matches:
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Sequence 799 from Patent BP1308459.
AX747274
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1. 1785
/organism="Homo sapiens"
/mol_type="mwkN"
/db_xref="taxon:9606"
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Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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KEYWORDS
SOURCE
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JOURNAL
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complement(join(87577. s88309,88753. .88871,88966. .89049,
91374. .91568,91663. .91779,92621. .92686,92779. .92982,
110273. .110350,112510. .112713))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="RP11-344H11.2-001"
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91374. .91568,91663. .91779,92621. .92686,92779. .92982,
110273. .110350,112510. .112713))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: ESTs: Em:BE798032.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82222 CAGAGAGCATTACCTTCATCTCTGGCTGTGAGCCGGCCCTTGAGTCCCCCACCTGCT
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join(82059. .83097,83683. .83757,84288.
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nidulans)"
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
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Isogai, T. and Yanamoto, J.

Direct Submission

Direct Submission

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kenail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Roomony, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5- & 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.

Location/Qualifiers
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FHESDLDLPEMGSGSMSSREIDVLIPKKLTELFSVHQIDELAKCTSDTVFLEKTSKIS
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HETWVGSGLSQDELIVQISQETTADAIARKLRPYGAPGYPASHDSSFQGTDTDSSGAP
LLQVYC"
                                                                                                                                                                                                                                           Tashiro, H., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Watsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Gehima, M., Burakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Magaes,T., Nomura,N., Xikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakaurra,Y., Ohara,O., Isogai,T. and Sugano,S. Complete sequencing and characterization of 21,243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SerProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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14702039
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      313 GCCTGCTCTGGCGACCCTGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCT 372
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Homo sapiens (human)
Homo sapiens
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ACCESSION
VERSION
KEYWORDS
SOURCE
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                          35244: gap of 100 bp
54710: contig of 19466 bp in length
54810: gap of 100 bp
72936: contig of 18126 bp in length
73036: gap of 100 bp
92988: contig of 19852 bp in length
92988: gap of 100 bp
108739: contig of 15751 bp in length
108839: gap of 100 bp
111738: contig of 2899 bp in length
                                                                                                                                                                            100 bp
of 16986 bp in length
100 bp
                                                                                                                                                            18058: contig of 18058 bp in length
18158: gap of 100 bp
35144: contig of 16986 bp in length
35244: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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fragment chain:1
clone=end:17
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18159. ..35144
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fragment chain:1"
35245. .54710
"note="assembly fragment:02786
fragment chain:1"
54811 ..72936
/note="assembly fragment:00223
fragment chain:2"
7037 ...5288
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Indels:
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92989. .108739
/note="assembly fragment:01122
fragment_chain:2"
108840. .111738
/note="assembly_fragment:02919
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Matches:
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vector_side:right"
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Best Local Similarity:
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Homo sapiens chromosome 1 clone RP3-426N7, 7 unordered pieces.
ALS92304
                                                                                                                                                          LeuArgThrProLeuArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCys 100
                                                                                                                                                                                                                                ProProAlaLeulleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro 120
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                                    552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg 180
                                                                                                                                                                                               492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      673 CCCCACCCATGCGACACCAGCCAGCAGCACTTGCCAGTAGTCCTCGTGGCTCCGAGG 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerThrileLeuSerMetSerArgThrTrpThrCysArgArgTrpAlaValAlaProCys 200
                                                                                                                                                                                                                                                                                                                                                                                                           733 AGTACTATTCTTTCCATGAGTCGGACCTGGCCGGAGATGGGCAGTGGCTCCATGT 792
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Mammalla; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Micat. Submission

Submitted (24-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                      61 AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
                                                                                                                                                                                CTGAGGACTCCACTGAGGGACTGCTGAAGCCAACTGGGCCAACGAGCACAAGGAGTGC
                                                                                                                                                                                                                                                                 493 cccccadcccrcarcarcarcccccadccadcagaraccaaccacaacrcaacca
                                                                                                                                                                                                                                                                                                                          AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
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Web Site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
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HTG; HTGS PHASE1; HTGS_CANCELLED
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
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Qy 1 SerProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly 20			Db 477 GCT1GCTTGGGGGGTGGGGGTGGGGGGGGGGGGGTGGCTTGCTTTGGGGGG	Db 537 TGCCGGGATTGCCTCCAGCGCTGTGTGGAGGCCTGTGTGGGGGATGCAGCCCTGCCTG	597	Db 657 GTGCCCCCGGCCCTGATCGTGCCACCCCCAGACCGGGGATGGCCAGGCGGGCTGCAA 716 Qy 118 erGlnProTrpAlaAlaAlaAlaAlaTeTroMetLeuSerSerIyaAlaSeTLeuCy91 138	Db 717 GTCAACCATGGCAGCAGCTTCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTA 776 Ov 138 leProThrArg-GlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHis 157		Qy 158 TrpProlleProHisProCysAsp-ThrAlaCysProAlaProLeuProValValLeuVa 177	Qy 177 lAlaProArgSerThrIleLeuSerMetSerArgThrTrpThrCysArgArgTrpAlaVa 197	Qy 197 lalaProCysArgaladluLysLeuMetCysSerSerSerArgSer 212	RESULT 9 AX535090 LOCUS AX535090 LOCUS DEFINITION Sequence 117 from Patent W002068633.	Homo sapiens (human) Homo sapiens		REFERENCE 1 AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C. TITLE Compositions and methods relating to lung specific genes and	JOURNAL Patent: WO 02068633-A 117 06-SEP-2002; Diadexus, Inc. (US)	urce	5.22e-22 Length:	Score: 1002.52 Marches: 206 Percent Similarity: 94.5% Conservative: 2
Db 95889 CAGAGAGCATTACCTTCATCTCTGGCTGAGCCGGCCCTTGAGTCCCCCACCTGCT 95948 Qy 41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla 60	95949 GCCTGCTCTGGGACCCTGGGTGTGGGTGGCTTGTTCTTCTTCTGCTTCGCCGGCTTCTGCTTCCGCGGCTGCT	OY 6.1 Alada VII EALASEESERAIS VAIGALEROVALCES SANDALARIOA ARICEDA ACCESSENTO 80	Qy 81 LeuargThrProLeuargGlyLeuLeuLeuLysProThrGlyProArgSerThrMetGluCys 100	Qy 101 ProProAlaLeuIleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro 120 Db 96129 CCCCCAGCCCTGATCGTGCACCCCCAAGCGGGATGGCCAAGGGCTCAAGTCAACCA 96188	Qy 121 TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCys1leProThr 140	Oy 141 ArgGlyProProGlnProLeuMetArgThrProAlaAlaArgSerHisTroIle 160 Db 96249 CGAGGGCCACCTCCCCAGCCCCTGATGCGACTCCTGCTGCAGAAGACCACTGGCCGATC 96308	Oy 161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg 180	181 SerThrileLeuSerMetSerArgThrTrpThrCysArgArgTrpAlaValAlaProCys	Db 96369 AGTACTATTCTATGGAGTCGGACCTGGACCTGCCGGAGATGGGCAGTGGCTCCATGT 96428 Qy 201 ArgalaGluLysLeuMetCysSerSerSerArgSer 212		9 AX535029 ION Sequence 56 ON AX535029	VERBION AX535029.1 G1:25461664 XEWORDS	REFERENCE 1 AUTHORS Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C. TITLE Compositions and methods relating to lung specific genes and	proteins JOURNAL Patent: WO 02068633-A 56 06-SEP-2002; Diadexus, Inc. (US)	FEATURES Location/Qualifiers 1. 1977 Source /organism="Homo sapiens" / mai = Homo sapiens but so sapiens so sap	/mo_rype="unablymed DNA" /db_xref="taxon:9606" ORIGIN	5.22e-22 1002.50 94.5%	Mismatches: Indels: Gaps:	US-09-989-890-238 (1-212) × AX535029 (1-1977)

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site: http://www.sanger.ac.uk
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Mouse DNA sequence from clone RP23-137L22 on chromosome 4, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        536
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Murinae; Mus.
1 (bases 1 to 193813)
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humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 4, 2003 this sequence version replaced gi:22474404.
---------------- Genome Center
Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                          SerProHisGlnAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euLeuArgThr-ProLeuArgGlyLeuLeuLysProThrGly-ProArgSerThrMetGl
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      404
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                              Query Match:
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AUTHORS
TITLE
JOURNAL
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Center code: SC

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMEL; Swi: SMISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

RR23-137122 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECTOR: pBACE3.6 Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

Location/Qualifiers
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104052 CAGAGAGTATCACCTTCATTTCAGGCTCTGCAGAACCAGCCAACGAGGCCCCCAACCTGCT
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Conservative:
Mismatches:
Indels:
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP23-137L22"
/clone_lib="RPCI-23"
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Best Local Similarity:
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/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse." /clone lib="MCI CGAP_Mam6" /lab_host="DH10B"
                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 16 Row: p Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19526881.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="wsapsphravapGGQTLRTLATWGQRVSPSFQALQNQPTSPQPA
ASSABADGVGTGGLBSASAAAGIACSBASAAPATALSEFPELKEEPERPUTM
VCPPARTVHPPAAGMAGSRPAWAAASATLMLSSKASLSTPTAMPPPOSLTWTPAARS
PWPSILIPHGTACLABSPTAPPAALRSTTPSWNRTWTCLRWAVAPCRAGRSTCLFSRS"
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 CAGAGAGTATCACCTTCAGGCTCTGCAGAACCAGCCAACGAGCCCCCAACCTGCT
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-989-890-238 (1-212) x BC006890 (1-1680)
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gene="1810019J16Rik"
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5. Gurognathi; Muroidea; Murinae; Mus.

1. (bases 1 to 1680)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Altschul,S.F., Zoeberg,B., Wagner,L., Schemmen,C.M., Schuler,G.D.,

Altschul,S.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Garai,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Sanilus,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length
                                                                       104412 GCCATGCCACCTCCCCAGTCCCTGACGTGGACTCCTGCTGCAGGAGCCCCTGGCCGAGC 104471
                                                                                                                                                                                                                                                                                104531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC006890 1680 bp mRNA linear ROD 29-JUN-2004
Mus musculus RIKEN cDNA 1810019J16 gene, mRNA (cDNA clone MGC:11921
                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                      141 ArgGlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle
                                                                                                                                                                                                                                                                             TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr
                                                                                                                                                                                                                               161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences
i. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         104592 CGAGCCGGGAGATCGACGTGCTTATTTTCAAGAAGC 104627
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                                                                                                                                                                                                                                                                                                                                                                                                                         ArgAlaGluLysLeuMetCysSerSerSerArgSer 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE:3599314), complete cds.
BC006890
BC006890.1 GI:13905189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci.
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Klausner, R.D., Collins, P. S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haish, R.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwant, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
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Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROD 15-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                        SerThrileLeuSerMetSerArgThrTrpThrCygArgArgTrpAlaValAlaProCyg 200
                                                                                                                                                               141 ArgGlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle 160
                                                                                                                                                                                               574 GCCATGCCACCTCCCCAGTCCCTGACGTGGACTCCTGCTGCAGGAGCCCCTGGCCGAGC 633
                                                                                                                                                                                                                                                                             161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg 180
                                                                                                                                                                                                                                                                                                                                    693
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC079148 11718 bp mRNA linear ROD 15-SEP-2(
Rattus norvegicus similar to hypothetical protein FLJ34633, mRNA
(cDNA clone MGC:94165 IMAGB:7128510), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
CCCCCAGCCCGGACCGTGCCCCCCCCCGGCCGGGATGGCCAGGGGCTCAAGACCCAGCA
                                                                                      634 CTCCTCCCACACGCCACAGCTTGCCTAGCACCTTCACCAACAGCCCCCGCGGCTCTGAGG
                                                         TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
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YPDVKLKGIPVYPYRHATSPVPDADSCCKEPLADPPPTRHSLPSTFTSSPRGSEEYYS
FHESDLDLPSPRGSGSNSRRETDVLIFKKLTELEVSHQIDELAKYTSDYPLEKTSKIS
FLISSITQDYHLDEQDSGBLLWGIIR ISTRKSRRRPQTSGGRSARSTAPAAAPDSGH
ETWVGSGLSQDELIVQISQETTADAIARKLRPYGAPGYPASQDSSFQGTDTDSSGAPL
                                                                                                                                   can be found
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GACVRSCSPCLSAGDPIEGSSEAAWAKEHNGVPPSPDRAPPSRRDGGKLKTSMGSSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPRPGQPRPSSGPPRLGPWERPTELCLETNDERSQPPPGRRTRR
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Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: d Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerProHisGlnAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="similar to hypothetical protein FLJ34633"
| protein id="AAH7948.1"
| db_xref="G1:5092713"
| db_xref="GeneID:313018"
                                                                                                                                                                                                                                                                                                                                                                                                                      tissue type="Kidney, rat (Brown Norway)" /clone lib="NIH MGC_236" /lab_host="DH10B"
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                         'clone="MGC:94165 IMAGE:7128510"
                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pExpress1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="GeneID:313018"
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="MGC94165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MGC94165"
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Best Local Similarity:
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Direct Submission

Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:22772470.

The sequence in this sasembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetry, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Soson, Y., Strong, R., Strong, S., Warren, J., Warren, R., Wai, X., Waite, R., Willson, R., Warren, R., Wai, X., Waite, R., Williams, G., Willson, R., Wacze, R., Wooden, H., Worley, K., Wright, R., Wu, J., Yabu, S., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
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Center project name: GEBU
Center clone name: GEBU
Center clone name: GEBU
Assembly program: Phrap; version 0.990329
Consensus quality: 225536 bases at least Q40
Consensus quality: 227458 bases at least Q30
Consensus quality: 22649 bases at least Q30
Estimated insert size: 235033; sum-of-contigs estimation
Ouality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: BCM
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Scillrogatell; Muclodea; Murinae; Murinae; Rattus.

Scillrogatell; Muclodea; Murinae; Murina, A., Addms, C., Alden, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Angalabechi, V., Angaranaike, D., Barber, M., Barnatead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnatead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barrell, K., Calderon, E., Cardenao, V., Carter, K., Cavazos, I., Ceasar, M., Cener, D., Couron, D., Chacko, J., Chen, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chacko, J., Chen, G., Corle, M., Cox, C., Coyle, M., Cree, A., D. Souza, L., Davis, C., Davis, C., Dunn, A., Durbin, W., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Bvans, C.A., Falls, T., Fan, G., Franer, C., Coxtell, R., Cox, C., Coyle, M., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Bvans, C.A., Falls, T., Fan, G., Franer, C.M., Gabisi, A., Gear, M., Henderson, N., Hernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Guevar, W., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevar, W., Hernandez, R., Hines, S., Hadun, S.L., Hodgson, A., Hoopues, M., Hernandez, R., Hines, S., Hadun, S.L., Hodgson, A., Hoopues, M., Mahleshwar, M., Loulseged, M., Lovan, J., Lewan, J., Lewan, J., Lewan, J., Lewan, J., Lau, M., Liu, Y., London, P., Longacre, S., Lopez, J., March, M., Mahlindar, M., Malloy, K., Mangum, A., Mannoud, M., Malloy, K., Mangum, A., Mannoud, M., Malloy, K., Mangum, S., Malloy, S., Mally, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, M., Mannoud, M., Malloy, W., Marken, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Marchan, S., Parks, K., Marken, M., Morris, R., Martines, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Peramon, C., Peramone, S., Paul, M., Morris, S., Mulosavijevic, A., Milosavijevic, A., Perez, A., Perez, M., Perez, S., Peres, P., Perez, D., Perez, M., Perez, S., Peres, P., Perez, J., Perez, M., Regis, R., Regish, R., Reilly, M., 
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Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 CTCCTCCCACACGCACAGCTTGCCTAGCACCTTCACCAGCAGCCCCCGTGGCTCTGAGG 715
                    476 CTCCCAGCCCAGACCGAGCACCCCCCAGCCGGGATGGGCAAAAGCTCAAGACCAGCA 535
                                                                                                                                                                           141 ArgGlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle 160
                                                                                                                                                                                                                                                                                                                                         596 GCCATGCCACCTCCCCCGTCCCCTGACGCGGACTCCTGCTGCAAGGAGCCCCTGGCAGACC 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerThrIleLeuSerMetSerArgThrTrpThrCysArgArgTrpAlaValAlaProCys 200
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 716 AGTACTATTCCTTCCATGAATCGGACCTGGACCTGCCCGAAATGGGCAGTGGCTCCATGT
                                                                                                    TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr
                                                                                                                                                                                                                                                                                                                                                                                                                        161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 ArgAlaGluLysLeuMetCysSerSerArgSer 212
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Dealer in Chases I to 249400.

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Ranzny, D.Marie, Metzker, M.Lee, Abramzon, S., Adama, C., Alder, J., Anglahach, V., Anglahach, D., Angodej, M., Baca, E., Baden, H., Balbarooks, S., Amin, A., Angulahach, D., Anyagi, A., Angodej, M., Baca, E., Baden, H., Balden, V., Angodej, M., Baca, E., Baden, H., Balden, V., Balden, M., Balden, D., Bandaranalke, D., Barber, M., Barantead, M., Benahmed, F., Biswalo, K., Glare, J., Cavera, C., Cavelan, C., Cavelan, C., Corder, D., Carter, M., Care, D., Chen, G., Chen, G., Corde, M., Care, C., Covela, M., Cree, A., D'Souza, L., Devila, M.L., Davis, C., Daramo, C., Coyle, M., Cree, A., D'Souza, L., Devila, M.L., Davis, C., Daramo, C., Ding, Y., Chan, S., Chu, J., Chare, C., Coyle, M., Carer, M., Carer, M., Carer, M., Carer, M., Carer, M., Carer, C., Ding, Y., Chan, C., Deramo, C., Ding, Y., Chan, S., Chu, C., Coyle, M., Carer, C., Coyle, M., Carer, M., March, M., Carer, M., March, M., Carer, M., March, M., Mayor, M., March, M., March
                                                                              AC118963 249406 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-180E4, WORKING DRAFT SEQUENCE.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus
1 (bases 1 to 249406)
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
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Direct Submission
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/mol_type="genomic DNA'
/db xref="taxon:10116"
                                                           /clone="CH30-11020"
2958 .3664
/note="clone boundary
clone end T7"
site: EcoRI
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end sequence: BH344813"
221493. .221592
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/note="clone_boundary
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Lucaryota; metazoa; Curonaca; Vertebrata; Euteleostcomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognachi; Muridae; Muridae; Murinae; Rattus.

I (bases 1 to 256017)

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alabrooks,S.L., Amaratunge,H.C., Are,J.R., Ayole,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Barbaria,J., Bowle,S., Bireva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.P., Carter,M., Cavacos,S.R., Chacko,J., Charez,D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Chen,Z., Chen,Z., Chon,Z., Chen,Z., Chon,Z., Chen,Z., Coyle,M.D., Dathorne,S.R., David,R., Davis,C., Blan,Y.C., Barnart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Farls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Garner,T., Garza,N., Gill,R., Gabisi,J., Gao,J., Garner,T., Garza,N., Gill,R., Garner,T., Hawes,A., Hamilton,K., Gorrell,J.H., Guevara,W., Gunaratne,P., Habe,S., Hamilton,K., Harris,C., Harris,C., Harris,K., Harr,M., Havlak,P., Hawes,A., Hamilton,K., Jackobson,B., Jia,Y., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Jucier,R., Lucier,R., Luna,R., Marinez,B., Li,J., Li,L., Li,Z., Lichearge,O., Liuu,C., Liu,J., Liu,W., Loulseged,H., Liz,J., Lucher,A., Lucier,R., Lucier,
      14233 GCCATGCCACCTCCCCCGTCCCTGACGCGGACTCCTGCTGCAAGGAGCCCCTGGCAGACC 14174
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*** SEQUENCING IN PROGRESS ***,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                  101 ProProAlaLeuIleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro
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                                                                                                  61 AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
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Rattus norvegicus (Norway rat)
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Rattus norvegicus clone CH230-1B9,
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:23269749.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the piaces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 249406: contig of 249406 bp in length.
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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/db_xref="taxon:10116"
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/note="wgs_contig"
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Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 13, 2002 this sequence version replaced gi:23267435.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Naylyen, A., Mguyyen, A., Naylyen, A., Naylyen, A., Naylyen, A., Naylyen, M., Nguyen, N., Nguyen, N., Oviedo, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Rickens, R., Primus, E., Pu, L.L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stone, M., Svateck, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Wang, S., Warten, R., Washington, C., Watlington, S., Williams, G., Williams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, S., Meleczyk, R., Wooden, S., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (05-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83721: contig of 83721 bp in length
83821: gap of unknown length
253567: contig of 169746 bp in length
253667: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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COMMENT

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155462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155161 CTCCTCCCACACACACACATACCTAGCACCTTCACCAGCAGCCCCCGTGGCTCTGAGG 155102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15221 GCCATGCCACCTCCCCGTCCCTGACGCGGACTCCTGCTGCAAGGAGCCCCTGGCAGACC 155162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155341 CTCĆCAĠĆĆCAGACCGAGCAĆĆĆĆĆAĠĆĆGCGĠĠĀTĠGGCAAAAGCTĆAAGACCAGCA 155282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 LeudrgThrProLeudrgGlyLeuLeuLy8ProThrGlyProArgSerThrMetGluCy8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155581 cacaccarcaccrrcarrrcagecrcrecagascagecaagececaaccrecr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ProProAlaLeulleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
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138
256017: contig of 2350 bp in length.
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Matches:
Conservative:
Mismatches:
Indels:

    .256017
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78781. .81213
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               location/Qualifiers
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83722. .83821
                                                                                                                                                                                                                                                                                                                                                                                                                                 _contig"
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653.00
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65.1%
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Best Local Similarity:
253668
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Pred. No.:
                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                        gap
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                 FEATURES
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 Qy
 181 SerThrIleLeuSerMetSerArgThrTrpThrCyeArgArgTrpAlaValAlaProCys 200

 Db
 155101 AGTACTATCCTTCCATGAATCGGACCTGCCCGAAATGGGCAGTGGCTCCATGT 155042

 Qy
 201 ArgAlaGluLysLeuMetCysSerSerSerArgSer 212

 Db
 155041 CGAGCCGTGAGATCGACGTGCTTATTTTCAAGAAGC 155006

Search completed: March 17, 2006, 06:11:49 Job time : 7588 secs

Fri

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Abto7645 Human bre Abx92075 Lung spec Abx92075 Lung spec Aaf66376 Novel hum Ac172571 M. xanthu Ac164503 M. xanthu Ac164503 M. xanthu Ad92194 Elmeria t Abx22078 Elmeria m Abz52078 Elmeria m Abz52078 Elmeria m Abz52078 Elmeria m Ac16476 M. xanthu Ac16476 P. xanthu Ac16476 P. yerich Abs73261 Human Gef Ad991713 Polyketid Acb8602 Streptomy Acb8602 Streptomy Acb8662 Streptomy Ach86659 Streptomy Ach86659 Streptomy Ach865905 Toxicity Ach2076 Toxicity Ach2078 Toxicity Ach2078 Toxicity Ach2078 Toxicity Ach2078 Toxicity Ach2078 Toxicity Ach2078 Streptomy Ach2078 Streptomy Ach2078 Streptomy Ach2078 Toxicity Ach2078 Toxicity Ach2078 Streptomy Ach2078 Streptomy Ach1184 Streptomy Ach1184 Streptomy Ach1184 Streptomy Ach2078 Toxicity Ach1186 Streptomy Ach1184 Streptomy Ach2078 Toxicity Ach2078 Streptomy Ach207
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                                                                                                                                                                                                                                                                                                                     AAF98697
ABS76388
AEB35261
ADQ91713
AEB87005
AEB86802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEB86862
AEB86659
AAK52397
AAZS5887
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ADP65796
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ABK63598
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ABX11642
ABL66291
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                                                        2914
29198
2914
864
6567
6567
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2703
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1799
4262
5142
5142
22533
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71989
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    Command line parameters:
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Abt13390 Breast sp
Add01260 Human nuc
Adb62645 Human cDN
                                                                                                                                                         (without alignments)
2402.916 Million cell updates/sec
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                                                                                                                                                                                                                                                          SPHQAAAPVDQTPRTLATMG......RRWAVAPCRAEKLMCSSSRS 212
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                                                                                                                                    March 17, 2006, 03:48:50 ; Search time 588 Seconds
                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                   - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                        4996997 seqs, 3332346308 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                       0.5
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ABT13390
ADD01260
ADB62645
                                                                                                                                                                                                                                                                                                                  Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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Match Length
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2392
1785
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Total number of

Searched:

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

sed

08

Minimum I Maximum I

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1134 1134 1128

Score

Result Š.

13211

Database :

Abx11642 Human ser Ab166291 Lung canc Adp13447 Renal cel

233 GCCTGCTCTGGCGACCCTGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCT 282

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The invention describes a new isolated polymucleotide (I) encoding a CC polypeptide with biological activity comprising: a nucleotide sequence of SEQ IN NOS: 1-567 (fully defined); a nucleotide sequence that hybridizes crot the sequence of (i) under stringent hybridization conditions; or a nucleotide sequence having greater than 99% sequence identity with the sequence of (i). Also described are: a(n) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polymucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 586-1134 (fully defined), where the polypeptide of is: a polypeptide encoded by (I); or a polypeptide encoded by a polymucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-567; a composition comprising the polypeptide of (3); an echod (or detecting (I) in a sample; a method for detecting the polypeptide of (3); and a sample; a method of producing the polypeptide of (3); and a collection of polymucleotides, where the collection comprising any of the sequences of SEQ ID NOS: 1-567. (I) is a polymucleotide with biological activity, which comprises are fully defined in the specification. The sequences of SEQ ID NOS: 1-567 encoding a polympeptide with biological activity, which comprises are fully defined in the specification. The sequences and methods are useful in diagnostics, forensic, and gene cother traits, in assessing biodiversity, and for producing many other types of data and products dependent on DNA and encode strong method are useful for tracting a disease, burns, stroke archimmus disarder viral infection or parcer. Whis sequences of data and products dependents or adsease, burns, stroke e.g. osteoporosis, osteoarthritis, periodontal disease, burns, stroke archimmus disarder viral infection or cancer. Whis sequences of sequences are useful for cancer. Whis equences of sequences are useful for genesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 AGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCAAGGACCCTGGCCACGATGGGC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .mmune disorders, viral infection, or cancer. This sequence encodes
                                                                                                                                                                                                                                                       polynucleotide encoding a polypeptide with biological activity, ful for treating a disease or disorder, e.g. osteoarthritis, burns, and peripheral disease, stroke, autoimmune disorders, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 CAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCT
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                                                                                                       Ma Y;
R, Chen l
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                                                                                                         Zhou P, N
Goodrich B
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                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 239; 500pp; English.
                                                                                                  ٥, رم
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                                                                                                     Zhang
Zhao Q
                                                                                                       Wang J, Wang ZW,
Xue A, Asundi V,
                    14-MAR-2003; 2003US-00389559
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1134.00
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                                                                                                                                                  Weng G, Boyle
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                                                                                                                                                                                          2005-417730/42
                                                                                                                                                                                                                                                       New polynucleotide
useful for treating
                                                              (NUVE-) NUVELO INC
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Best Local Similarity:
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P-PSDB; AEA20112.
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                                                                                                       Tang TY,
Ghosh M,
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The invention relates to a novel isolated nucleic acid molecule comprising: a sequence encoding a sequence comprising 11-1518 amino acids; a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60% identity with the 11-1518 amino
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                       LeuArgThrProLeuArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCys
                                                                                                             ProProAlaLeuIleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro
                                                                                                                             CCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGATGGCCAGCGCTCAAGTCAACCA
                                                                                                                                                                                  TGGGCAGCAGCTTCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACC
                                                                                                                                                                                                                        ArgGlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle
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                                                                      CTGAGGACTCCACTGAGGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breast specific related polynucleotide SEQ ID No 105.
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                                                                                                                                                                                                                                                                                                                                                                                                                     CGAGCCGAGAATTGATGTGCTCATCTTCAAGAAGC 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВÞ.
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acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polynucleotides of the invention can be used to treat disorders by gene therapy. This polynucleotide represents a breast specific related sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403
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                                                                                                                                                                                                                                                                                                                                                                                            41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
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Matches:
Conservative:
Mismatches:
                                                                                                     468 G; 348 T; 0
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                                                                                                     BP; 344 A; 553 C;
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Best Local Similarity:
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The present invention describes human nucleic acid-associated proteins designated NAAP-1 to NAAP-57. The human NAAPs have cytostatic, antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective, antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective, antiarteriosclerotic, anticonvulsant, noctropic, neuroprotective, cantinflammatory, ophthalmological, thyromimetic, antiparasitic and fungicide activities, and can be used in gene therapy. The NAAP protein can polynuclectide sequences can be used in diagnosing, treating and preventing diseases or conditions associated with the decreased conversapression or oversapression of NAAP, such as cell proliferative diseases (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (Parkinson's disease, Alzheimer's disease, stroke, epilepsy), developmental disorders (renal tubular acidosis, anaemia, glaucoma, CC hypothyroidism), autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis, arthritis) and infections (e.g. bacterial, viral, viral, from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human nucleic acid-associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
human; nucleic acid-associated protein; NAAP; cytostatic; antiatreriosclerotic; anti-HIV; antiallergic; cerebroprotective; antiparkinsonian; anticonvulsant; nootropic; neuroprotective; antiinflammatory; ophthalmological; thyromimetic; antiarthritic; hepatchropic; antibacterial; virucide; protozoacide; antiparasitic; fungicide; gene therapy; cell prollferative disease; cancer; atherosclerosis; hepatitis; neurological disorder; Parkinson's disease; Alzheimer's disease; stroke; epilepsy; developmental disorder; renal tubular acidosis, anaemia; glaucoma; hypothyroldism, autoimmune disorder; inflammatory disorder; ADS; allergy; atopic dermatitis; arthritis; infection; gene; ss.
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Merling BM, Forsythe IJ, Gorvad AB, Griffin JA,
Bre R. Lal PG, Lee EA, Lee SY, Li JX, Marquis L,
Richardson TW, Sprague WW, Swarnakar A, Tang YT;
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AE, Khare R, Lai ...
T. Richardson TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2002; 2002US-0347633P.
25-JAN-2002; 2002US-0351749P.
22-FEB-2002; 2002US-035949BP.
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Ramkumar J,
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Length: Matches: Conservative: Mismatches: Indels:

1.13e-35 1134.00 100.0% 100.0% 100.0%

Best Local Similarity:

Query Match: DB:

Percent Similarity:

Alignment Scores:

(1-2392)

US-09-989-890-238 (1-212) x ADD01260

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| LeuargThrProLeuargG]yLeuLeuLysProThrG]yProArgSerThrMetG]uCys 100
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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SerProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly
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tissue regeneration; cell regeneration; membrane protein;
signal transduction-related protein; transcription-related protein;
osteoporosis; neurological disease; cancer; tumour.
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/*tag= a /product= "Clone KIDNE20157100 protein"
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The invention discloses a polynuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel

CC polypeptides. Also claimed is a polypeptide encoded by the polypeptide or or its partial peptide, immunologically assaying the polypeptide or peptide or peptide or peptide or coff the polynucleotide, immunologically assaying the polypeptide or peptide or coff the polynucleotide by contacting the polypeptide or peptide or with the antibody of the encoded protein, and observing the binding compressible manner and an antisense polynucleotide. The oligonucleotide is useful as a primer for synthesising the polynucleotide, or as a probe contact of a useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and many disease-related companies for regulation of their expression and activity, or as targets of genes may be included in them, for developing a diagnostic marker or regeneration. Membrane proteins, signal transduction-related proteins, creameration. Membrane proteins, signal transduction-related proteins, creameration. Membrane proteins, disease-related proteins and genes concoding them can be used as indicators for diseases (e.g. osteoporosis, curvicion-related proteins, disease-related proteins and genes concoding them can be used as indicators for diseases (e.g. osteoporosis, curvicions) patent is not respression of the encoded protein to treat diseases. The concoding them can be used to replace the encoded protein to treat diseases. The concoding them can be used to represented in the printed specification, but an encoded protein or the activity or expression of the encoded protein to treat diseases. The concoding them can be used to respression of the encoded protein printed specification, but and the printed or respression of the encoded protein or the activity or expression of the encoded protein printed specification and the printed or the activity or expression of the encoded protein or the activity or each or the activi
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                                                                                                                                                                                                                                                                                           useful for developing a diagnostic their expression and activity, or
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Otsuki T, Wakamatsu A, Sato H, Ish
Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
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                                                                                                                                                                                                                                                                                                New polynucleotides and polypeptides, marker or medicines for regulation of
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                                                                                                                                                     ArgGlyProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle 160
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                                                                                                                                                                                                                                             CCCCACCCATGCGACACAGCCTGCCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGG
                                                                                                    CGAGGGCCACCTCCCCCAGGCCCCTGATGCGGACTCCTGCTGCAGGAGCCACTGGCGGATC
                                    CCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGATGGCCAGCTCAACCA
                ProProAlaLeulleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro
                                                                                  TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr
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Alignment Scores

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The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                     Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal; gene; ss.
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                                                    197 1A1aProCysArgAlaGluLysLeuMetCysSerSerSerArgSer
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                                                                                                                                                                                                            The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (SI), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence
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rcia V, Jones LW, Strache-Crain B;
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Kennedy GC,
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Kasaema A, Reinhard C, Randazzo F,
Drmanac R, Crkenjakov R, Drmanac S,
Leshkowitiz D, Kita D, Garcia V, J
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Crkenjakov B, Garcia V,
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99US-0142311P.
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The present sequence is one of 3351 sequences in a library of human polymucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies to produce probes for detection of transcription levels. Ribbozymes or antisense oligonucleotides can be used for chromosome mapping of the polymucleotides. The probes can be used for chromosome mapping of the polymucleotides and for detection of transcription levels. Ribbozymes or antisense oligonucleotides can be generated. The polymucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polymucleotides, polypeptides and preventive them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242
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mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences.
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                                                                                    Claim 9; Page 854; 1046pp; English.
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The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a plant by construct for expression of a nitrite reductase gene in a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest in records for SEQ IDs 1-1849 represent a set of 1849 contig and singleton sequences comprising coding sequences, but replication elements, promoters and other regulatory elements from the genome of the bacterium Maycoccous xanthus. Note: The sequence data for this patent did not form part of the printed specification, but was
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                                                                                                                                                                                                                                                                                                                                          The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest, and for constructing mutations in a gene of interest sequence given in records for SEQ IDS 1850-9691 represent a set of about 7842 genes or partial genes from the genome of the bacterium Mxyococcus xanthus. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
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                                                                                                                                                       ProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGlyGln 21
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                       Sequence 9198 BP; 1247 A; 3175 C; 3389 G; 1387 T; 0 U; 0 Other;
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The present invention describes DNAs encoding hair keratin-associated proteins (KAP) of human origin, which bind to hair keratin. Also choteins (KAP) of human origin, which bind to hair keratin. Also described: (1) DNA encoding KAPs of mouse origin; (2) proteins encoded by the human and mouse DNA, and their partial peptides, and proteins derived from them by addition, deletion and/or substitution of one or more amino acid residues; (3) DNA hybridising to the DNA encoding KAP; (4) peptides (5 acid residues; (3) DNA hybridising to the DNA encoding KAP; (4) peptides (6) accepted and peptides; (7) recombinant proteins and peptides; (8) expression vectors containing the DNA encoding KAP; (9) host cells transformed by these vectors; (10) non-human animals which these antibodies; (8) expression vectors containing the DNA encoding KAP; (9) host cells transformed by these vectors; (10) non-human animals which care knockout animals for KAP or which overexpress KAP; (11) screening substances promoting or inhibiting the binding of KAP; composing using KAP or promoting or inhibiting the expression of KAP; composing using KAP or their partial peptides or cells expression vectors for them; (12) compositions containing these compositions containing these compositions containing these compositions for them; or host compositions (such as hair and beard growth improvers, hair colourants or growth promoters. The KAPs are useful as active ingredients in toiletry compositions (such as hair and beard growth improvers, hair colourants or growth promoters. The KAPs are useful as active ingredients in toiletry compositions (such as hair and beard growth improvers, hair colourants and hair invention.

Compositions or has been are located on chromosome 21, more exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                     gene;
                                                                                                                                                                                                                                                                                            hair; keratin-associated protein; KAP; human; keratin; toiletry; therapeutic; hair growth promoter; hair disorder; chromosome 21;
                                                                                                                                                                                          Human hair keratin-associated-protein encoding cDNA SEQ ID NO:5.
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P-PSDB; ADJ92147.
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(revised)

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                                                                                                                                                                       Antigen; vaccine; poultry; fowl; avian coccidiosis; immunization; ss
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protecting poultry against coccidiosis.
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                                362 GCTCCTCCAGCACCTGCGCCCCTCTTCTCCGGGCAGCTCCTCAGCATTGCCGCCAGAG 303
                                                                                         ---ProTrpAlaAlaAlaSerAlaThrProMetLeuSerSerLyBAlaSerLeuCyBIle 138
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                                                                                                                                                                                                                                                                       CDNA encoding the GX5401 antigen to identify clones encoding extensions of the GX5401 coding sequence. Several plaques reactive with the CDNA were identified. DNA from clone number 533 was sequenced. This analysis showed that the coding sequence in this clone overlaps with the GX5401 coding sequence and extends that sequence toward the N-terminal coding region. Analysis of the new sequence together with the GX5401 antigen coding sequence reveals an open reading frame encoding an Elmeria protein coding sequence reveals an open reading frame encoding an Elmeria protein coding sequence and extends that sequence for protein reading frame encoding a potential signal sequence for protein secretion. The coding sequence for this antigenic protein is given in AAN93324. Also new are an expression vector contg. the cloned gene, host cells transformed with the vector, and AP encoded by the cloned gene. The transformed cells are used in a vaccine to immunise birds against avian coccidiosis. By labelling the peptides, they can be used as a type-specific probe. The AP may also be used in an assay to detect Ab against the coccidia. The Abs are used to indentify transformed cells contg. the DNA. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                             Cloned gene or fragment encoding antigenic protein - which binds with antibodies against avian coccidia, and transformed cells used in vaccine.
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The present invention describes a nucleic acid (I) comprising a sequence encoding a 250 kDa polypeptide from Sporozoites/Merozoites of Eimeria maxima or its homologue or complement. Also described: (1) a vector comprising the nucleic acid; (2) a host cell comprising the vector; (3) a plasmid comprising the nucleic acid; (4) a transformed cell comprising to plasmid comprising the nucleic acid; (6) a transformed cell comprising or the nucleic acid; (5) producing a recombinant E. tenella, E. acervulina, c. E. necatrix, E. pracox; E. maxima, E. mitis or E. brunetti or a necorganism expressing an immunologically cross-reactive antigen; (8) immunising a subject against infection by Eimeria, or a microorganism expressing an immunologically cross-reactive antigen; (9) conferring upon capturessing an immunologically cross-reactive antigen; (9) conferring upon a newborn subject of an avian species maternal immunity against infection by Eimeria; (10) a fertilised egg from an avian species having an air sac, where the air sac is inoculated with the vaccine; and (11) reducing the output of Eimeria occytes in facces from a newborn subject of an avian species (1) has antiparasitic activity and can be used in a vaccine and in gene therapy. The nucleic acid is useful for preparing a vaccine against E. tenella, E. acervulina, E. necatrix, E. pracecox, E. maxima, E. mitis or E. brunetti infection. The present sequence, which is represents a 250 kDa antipen protein homologous DNA sequence.
                                                                      5948 CCAGAGCCTCCTCCTCCGCCGGCACCTGCGCCCCCTCTTCTCCGGGCAGCTCCTCAGCA 5889
---ProTrpAlaAlaAlaSerAlaThrProMetLeuSerSerLyBAlaSerLeuCyBIle 138
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BE901537 GI:10390818
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov

Plate: LLCM842 row: g column: 05

High quality sequence stop: 668.

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CGAGGGCCACCTCCCCAGCCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATC 583
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NH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BQ691555 917 bp mRNA linear EST 15-JUL-2002 AGENCOURT 8341018 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249453 5', mRNA sequence.
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 535.
Location/Qualifiers
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1 (bases 1 to 917)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
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BQ691555.1 GI:21816871
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                                                                                                                                                      Chordata; Craniata; Vertebrata; Buteleostomi;
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Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW810 row: d column: 06
High quality sequence stop: 752.
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                                                                                                                                                                                                 Hominidae; Homo.

1 (bases 1 to 1015)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo:
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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/db_xref="taxon:9606"
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/clone=lib="NIH MGC_110"
/clone=lib="NIH MGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAnoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University coff California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini;
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Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
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Mismatches:
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Submitted (17-AUG-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DRFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKPZ (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DRFZ666B1777) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzbd.de/cgi-bin/products/cl.cgi?CloneID=DKRZp686B1777
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
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/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/cloine="prostate"
/cloine="pib="686 (synonym: hlcc3). Vector pSport1_Sfi; host DH10B; sites Sfilk + 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR749558 1671 bp mRNA linear HTC 19-AUG-2004
Homo sapiens mRNA; cDNA DKRZp686B17277 (from clone DKFZp686B17277).
CR749558
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/protein_id="CAH18355.1"
/db_xref="G1:51476785"
/translation="MPRPGHPRPASGPPRLGPWBRPTELCLETYDKPPQPPPSRRTRR
                                                                                140
                                                                                                                              466
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1 (bases 1 to 1671)

Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
ArgGlyProProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle
                                                                                                                                                                                                          SerThrIleLeuSerMetSerArgThrTrpThrCysArgArgTrpAlaValAlaProCys
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/codon_start=1
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Direct Submission
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Homo sapiens
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sapiens cDNA 5' end, mRNA sequence.
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                                         AA316608
AA316608.1 GI:1968936
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                                                                                   Homo sapiens (human)
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/note="0ligo dT_primed, full-length enriched cDNA library
from MoSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
Control human ES cell growth and differentiation
Nat. Blotechnol. 22 (6), 707-716 (2004)
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                                                                                                                                                                                                                                                                                                  /tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
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                                                                                                                         Regenerative Medicine
Geron Corporation
730 Constitution Drive, Menlo Park, CA 94025,
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 753 Std Error:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               753
157
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Hominidae; Homo.

I (bases 1 to 510)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinetock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Fischer, C., Hastings, G.A.,

Nozak, D.L., Kunsch, C., Hungluu, J., Li, H., Meissner, P.S., Olsen, H.,

Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Baymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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For clone availability, additional sequence and expression

For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.
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/organism="Homo sapiens"
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/mol_type="mRN"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
TEL: 3018699056
Fax: 3018699423
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87 AGCCCCCACCAAGCCGCCGCACCCGTAGACCCAGAACCCCTGGCCACCATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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                                                                                                                                    ProGInProLeuMetArgThrProAlaAlaArgSerHisTrpProIleProHisProCys 164
                        105 IleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnProTrpAlaAlaAla 124
                                                      181
                                                                              SerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThrArgGlyProPro 144
                                                                                                          241
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                                                                                                                                                                                         AspThralaCysProAlaProLeuProValValLeuValAlaProArgSerThrIleLeu 184
                                                                                                                                                                                                                                             CTGAGGGGACTGCTGAAGCCAACTGGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTG 121
                                                                                                                                                                                                                    302 GACACAGCCTGCCCAGCACCTTTGCCAGTAGTCCTCGTGGCTCCGAGGAGTACTATTCTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 583)

2 uzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                182 TCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACCCGAGGGCCACCT
                                                                                                                                                              242 ccccasccccrcarscscarcrccrscrscaassasccarrsccsarccccarsc
                                          ATCGTGCACCCCCCAGCCGGGATGGCCAGCGGCTCAAGTCAACCATGGGCAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
A-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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790.00
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Best Local Similarity:
Query Match:
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601593919F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3947885 5',
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EcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/XhoI sites using the following 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 CCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGATGGCCAGCGGGTCAAGTCAAGTCAAGTCAACCA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr 140
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCW810 row: e column: 06
High quality sequence stop: 615.
Location/Qualifiers
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                                    147 CAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCT
                                                                                                                                                                                                                                                          61 AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
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GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
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1 (bases 1 to 633)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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/clone lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunato, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-1384-format Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new g Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues.
Please visit our web site for further details
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
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/db_xref="taxon:I0090"
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 TCTACTGAGGATTCCACTGAGGGGACTGCTGAAGCCAACTGGTGCCAAGGAGTCACAATG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 etGluCysProProAlaLeuIle-ValHisProPro-AlaGlyGlyMetAlaSerGly-S 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 GTAGTGACCCCCAGCCCTGATTCGTGCACCCCCCAGACGGGGGATGGCCAGCGGTG 410
                                     insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 laAlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAla-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 sLeuLeukrgThrProLeukrgGlyLeuLeuLysProThrGly-ProArgSer---ThrM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
            Size-selected >500bp for average orary constructed by Ling Hong in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230011M17 product:hypothetical protein, AKO51860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuCysIleProThrArg-GlyProProGlnProLeuMetArgThrProAla-AlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerProHisGlnAlaAla-ProValAsp-GlnThrProArgThrLeuAlaThrMetG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 CTGTGTATCCCTACCCGAGGGTCCACCTCCCCAGCCCCTGATGCGGACTCCTGCTGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 lyGlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProProA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AlaAlaGlyIleAlaSerSer-AlaValGluProValCysGlyAspAlaAlaProAlaCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erSerGln-ProTrpAlaAlaAla---SerAlaThrProMetLeuSerSerLysAlaSer
                                                                                                                                                                                                                                                           623
164
17
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1-623)
                  adaptor: GGCACGAG(G).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTC; CAP trapper.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                     9.56e-31
687.00
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82.4%
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                                                                                                                                                                                                                                  Alignment Scores:
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KEYWORDS
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Euteleostomi;

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Sciliognathi, Murciace; Murine; Mis.

Sciliognathi, Murciace; Murine; Mis.

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,T., Osato,N., Saito,R., Yazuki,H., Yamanaka,I.,

Kiyosawa,H., Yaqi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Marsuda,H.,

Batalov,S. Beisel,K., Frazer,K.S., Gasterland,T.,

Fletcher,C.P., Forrest,A., Frazer,K.S., Gasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J. Grimmond,S.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

Kurochkin,I.V., Lee,Y., Lee,Y., Lee,Y., Lensaka,R., Malott,D., Rayalott,D.R.,

Muntais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pescole,G.,

Petrovsky,N., Pillai,R., Pontius,Ju., Ol., Ol., Ramachandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shinada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Tesadale,R.D., Tomita,M.,

Verardo,R., Wagner,L., Wahleredt,C., Wang,Y., Watanabe,Y.,

Hayatsu,N., Hirozane-Kishikawa,T., Yonno,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Azawa,K.,

Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imoton,R., Lander,R.S.,

Rogers,J., Blirney,B. and Hayashizaki,R., Sasaki,D., Shibata,K.,

Rogers,J., Birney,B. and Hayashizaki,R., Sasaki,D., Shibata,R.,

Rogers,J., Birney,B., and Hayashizaki,R., Sasaki,D., Shibata,R.,

Rogers,J., Birney,B., and Hayashizaki,R., Sasaki,D., Shibata,R.,

Rogers,J., Shiraki,T., Sakai,R., Shiraki,R., Sasaki,D., Shibata,R.,

Rogers,J., Shiraki,R., Sakai,R., Shiraki,R., Sasaki,D., Shibata,R.,

Rogers,J., Shiraki,R., Sakai,R., Shiraki,R., Shiraki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remail: genome-resegec.riken.jp, URL.http://genome.gec.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hixozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Makamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohaato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Pax: 81-45-503-9216
                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buto
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 420, 563-573 (2002)
   GI:27118783
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VERSION
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                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                                                               /proteIn_id="BAC34790.1"
/db_xref="C1:26342256"
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WWPGSLGSGLLVRRPGGGWERSSFVSRHNSDGLSQGPKRGGPDDGRGCPGLGMAQSMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1190 CAGAGAGTATCACCTTCATTTCAGGCTCTGCAGAACCAGCCAACGAGCCCCCAACCTGCT 1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProProAlaLeuIleValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnPro 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla 40
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1009 bp mRNA linear EST 16-DEC-200

WHOSTOLING CONA Clone 1810019J16 5', mRNA sequence.

BY707606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
                                  /note="unnamed protein product; hypothetical protein
(evidence: decoder, Longest-ORF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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Human Genome Sequences Mam. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Nouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoneda,Y., Inhikawa,T., Ozawa,K., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-UL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
BINDING PROTEIN (TBP)-ASSOCIATED FACTOR, RNA FOLYMERASE 130KD homolog [Mus musculus], full insert sequence.
                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bute
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                  cloning
                                                                                                                                                                                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                      Mus musculus (house mouse)
Mus musculus
                                                           AK007551.1 GI:12841167
HTC; CAP trapper.
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                                                                                                                                                                   /tissue_type="pancreas"
/dev_stage="10 day old"
pancreas" pancreas (10 day pancreas)
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'organism="Mus musculus"
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                                                                                                      db_xref="taxon:10090"
clone="1810019J16"
    cocation/Qualifiers
                                                               /mol_type="mRNA"
/strain="C57BL/6J"
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Yokohama

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/clone="IMAGES:712110110"
/clone="IMAGES:7121141"
/tissue_type="lung, pooled"
/lab host="DH10B TonA"
/lab host="DH10B TonA"
/clone lib="NHH MGC_232"
/note="Organ: lung, Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled lung tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80c for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
5-pGACTAGTTCTAGATCGCAGCGCCCCCC(T) 25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.3 kb. This primary library is normalized (non-normalized primary library is NIH MGC_231) and was constructed by Express Genomics (FrederIck, MD). Note: this is a NIH_MGC_library."
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Rattus norvegicus (Norway Lat.)

Rattus norvegicus (Nordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognachi; Murcidea; Muridae; Murinae; Rattus.

1 (bases 1 to 783)

1 (bases 1 to 783)

1 (bases 1 to 783)

2 National Institutes of Health, Mammalian Gene Collection (MGC)

1 Unpublished (1999)

2 Contact: Daniela S. Gerhard, Ph.D.

3 Contact: Daniela S. Gerhard, Ph.D.

4 Contact: Daniela S. Gerhard, Ph.D.

5 Contact: Daniela S. Gerhard, Ph.D.

6 Contact: Daniela S. Gerhard, Ph.D.

8 National Cancer Institute / NIH

8 National Cancer Institut
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/db xref="taxon:10116"
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/proteIn_id="BAC25177.1"

db_xref="G1:26357449"

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GVPPSPDRAPPSRRDGGRLKTSKGSSFSYPDVKLKGIPVYPYRHATSPVPDVDSCCKE
PLABPPPTRHSLPSTFYNSPRGSBEYYSFHESDLDLPEMGSGSMSSREIDVLIFKKLT
ELFSVHQIDELAKCTSDTVFLEKTSKISDLISSITQDYHLDEQDAEGRLVNGIIRIST
RKSRSRPPTSEGRARSTAPAAAPDSGHBTMLGSGLSQDELTVQISGETTADAIARKL
RPYGAPGYPASQDSSFGTDTDSSGAPLLQVYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pancreas"
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/dev_stage="10 day old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product; SIMILAR TO TATA BOX BINDING PROTEIN (TBP)-ASSOCIATED FACTOR; RNA POLYMERASE II, Cl, 1300 homolog [Mus musculus] (SPTR [092200, evidence: PASTY, 97.2%ID, 100%length, matche49)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAla-CysLe
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/strain="C57BL/6J"
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/tissue type="motion"
/lab_host="nHi08 (phage-resistant)"
/lang tumors with a Not I - oligo(dT) primer [5,
retraccharcheancheanted (dT) primer [5,
retraccharcheancheanted (dT) primer [5,
retraccharcheanted cDNA was ligated to Eco RI adaptors
(phamacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pr773 vector. Library
went through one round of normalization, and was
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DNA Sequencing by:Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov http://image.llnl.gov ncolumn: 23 High quality sequence start: 29 High quality sequence stop: 909.
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Matches:
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/mol type="mxRA"
/strain="Czech In"
/db xref="taxon:10090"
/clone="IMAGE:5119942"
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1 (bases 1 to 1040)
1 (bases 1 to 1040)
Nath-MCC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Tisane Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                 Length:
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Search completed: March 17, 2006, 07:14:01 Job time : 3879 secs

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Title: Perfect score:

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Sequence 1, Appli
Sequence 13231, A
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Sequence 420, App
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Sequence 799, Application US/10104047
GENERAL INFORMATION:
TITLE OF INVENTION: No. 6943241el full length CDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
FRIOR FILING DATE: 2002-03-25
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US-09-568-102-1

US-09-568-480-1

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US-09-568-472-1

US-09-949-016-13231

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US-09-949-016-650

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US-09-902-540-11339

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US-09-902-540-1339

US-09-902-540-1155

US-08-457-6463-6

US-08-457-343-4

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US-08-723-34-6

US-08-723-33-4
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Best Local Similarity:
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      TYPE: DNA
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Q= AbsS/MES = Pool/US09989990/runat 16032006_095249_16649/app_query.fasta_1

Q= AbsS/MES = Pool/US09989990/runat 16032006_095249_16649/app_query.fasta_1

DB=1ssued_Patente NA - OFMT=fastap - SUFFIX=p2n.rni - MINMATCH=0.1 - LOOPCIL-0

-LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi

-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MIN=0 - ALIGN=15

-MODE=LOCAL - OUTFNT=pto - NOFM+ext - HEAPSIZE=500 - MINIEN=0 - MAXLEN=20000000

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-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THRRADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6

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Sequence 9034, Ap
Sequence 2939, Ap
Sequence 1207, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
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                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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| CGM2_6/ptodata/1/ina/5_COMB.Beq:*
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| CGM2_6/ptodata/1/ina/6A_COMB.Beq:*
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| CGM2_6/ptodata/1/ina/PP_COMB.Beq:*
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US-09-902-540-9034
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US-09-443-501A-2
US-09-724-89A-2
US-09-734-876-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1303057 seqs, 888780828 residues
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ProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGlyGln 21
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; Sequence 966, Application US/09902540
; GENERAL INFORMATION
; GENERAL INFORMATION
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10 (15849)B
; CURRENT APPLICATION UNMERR: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
                                                                                                           -----CysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAla
                                                                                                                          22 ArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAlaAla
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                                                                                                                                                                                                                     73 GlyAspAla----ThrProLeuArg
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APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Blatcr, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: WAXCOCCUB xanthus Genome Sequences and Uses Thereof File REPERSICE: 38-10(1584)9 CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: US/09/902,540

PRIOR PILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

SEQ ID NO 90:4

LENGTH: 1716
                                                                                                                                                                               LeuArgThrProLeuArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCys
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               GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProProAla
                              CAGAGAGCATTACCTTCATCTCTGGCTCTGAGCCGGCCCTTGAGTCCCCCACCTGCT
                                                                   41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
                                                                                    GCCTGCTCTGGCGACCCTGGGTGTGGGGAGTGGTGCCGGGCTGCCTTCTGCTTCTGCTTC
                                                                                                                       AlaGiyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
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                                                                                                                                                                                                                                                               493 CCCCCAGCCCTGATCGTGCACCCCCCAGCGGGGGATGGCCAGCAGCTCAAGTCAACCA
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US-09-902-540-9034/c
; Sequence 9034, Application US/09902540
; Patent No. 6833447
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERRNE: 38-10[15849]B
CURRENT APPLICATION NUMBER: 2001-07-10
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2939
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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--AspAla 75
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 71989
64 AlaSerSerAlaValGluProValCysGly
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; Sequence 2, Application US/09443501A
; Patent No. 6303342
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APPLICANT: Tang, Li
APPLICANT: Ziermann, Rainer
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Katz, Leonard
Khosla, Chaitan
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                                                                  1075 GCCGGCCTCCCACCGCCCCACCAGCGCCACCGTGGCCGGGGCCATGCCTCCCGCCTTGC 1016
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFREENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1207
LENGTH: 23417
                                                                                                                                                             .015 GGGCCCGTGCGCGCTGCTCTTGCGACAGCGCCTCCAGCAGCGCCCCCATGGAGGCGA
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OTHER INFORMATION: unsure at all n locations
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ORGANISM: Myxococcus xanthus
FEATURE:
NAME/KEY: unsure
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Best Local Similarity: ,
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Sequence 2, Application US/09724889A
Patent No. 6858411
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APPLICANT: Kosan Biosciences, Inc.
APPLICANT: Julien, Bryan
APPLICANT: Katz, Leonard
APPLICANT: Khosla, Chaitan
APPLICANT: Tang, Li
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Best Local Similarity:
Query Match:
Alignment Scores:
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TITLE OF INVENTION: Recombinant Methods and Materials for Producing TITLE OF INVENTION: Recombinant Methods and Materials for Producing TITLE OF INVENTION: Epothilone and Epothilone Derivatives SITLE REPREBRENCE: 30062-20031.00
CURRENT APPLICATION NUMBER: US/09/724,889A
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-11-19
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR PLILING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-03
PRIOR PLILING DATE: 1999-03-01
PRIOR PLILING DATE: 1999-03-01
PRIOR PLILING DATE: 1999-03-03
PRIOR PLILING DATE: 1999-01-03
PRIOR PLILING DATE: 1998-11-20
PRIOR PLILING DATE: 1998-11-20
PRIOR PLILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRANCE PLILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
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17586 CCCCCTCGCTCTTGCCCGACAGCACCAAAAGCTCCGCCGAGCGCTCCGGCGCGGCAGGCC 17527
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                                                                                                71 ValCysGlyAspAlaAlaProAlaCysLeuLeuArgThrProLeuArgGlyLeuLeuLys 90
         ------LeuProSerAlaSerAlaAlaAlaGlyIleAlaSerSerAlaValGluPro 70
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APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: Ligon, James
APPLICANT: APPLICANT: Strkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
APPLICANT: Gerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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Patent No. 6121029
GENERAL INFORMATION:
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                                                                      169 ProAlaProLeuProValValLeuValAlaProArgSerThrileLeuSerMetSerArg
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                                                                                                                   -----CysSerGlyAspProGlyCysGlySerGlyAlaGly-------
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PRIOR PELICATION NUMBER: US/09/443,501
PRIOR PELING DATE: 1999-11-19
PRIOR PELING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
PRIOR PELING DATE: 1999-03-03
PRIOR FILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-02-10
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PRIOR PILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-02-10
SEQ ID NO: SEQ ID NOS: 22
LENGTHARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 71989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kosan Biosciences, Inc
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17406 CCAACGCGAGCG 17395
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APPLICANT: Katz, Leonard
APPLICANT: Khosla, Chaitan
APPLICANT: Tang, Li
APPLICANT: Ziermann, Rainer
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23681 CCCACGACCGCCACAGCGCCGTCAGCGCGTACTCCACCGCGAAGAGGCGCGGGCTGGG--- 23625
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; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-568-102-1
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                                 -----CysSerGlyAspProGlyCysGlySerGlyAla------
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APPLICANT: Ligon, James
APPLICANT: Molnar: Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Jevon
APPLICANT: TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
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CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
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Sequence 1, Application US/09568102
Patent No. 6346404
GENERAL INFORMATION:
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APPLICANT: Zirkle, Ross
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Cyr, Devon
TITLE OF INVENTION: GENES POR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
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Matches:
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Best Local Similarity:
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US-09-568-480-1/c
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                                         APPLICANT: Cyr, Devon
APPLICANT: Goellach, Joern
TITLE COF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REPERENCE: 430582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 68750
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Matches:
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ORGANISM: Sorangium cellulosum
US-09-567-969-1
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165.00
35.7%
28.7%
14.6%
Molnar, Istvan
Zirkle, Ross
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	23198 CCCCTCGCTCTTCCCGGCGCGCGGCGCGGCGCGCGCGCG	APPLICANT: Cyr, Devon APPLICANT: Goerlach, Joern TITLE OF INVENTOR: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES TITLE OF INVENTOR: 4-30582A TITLE REPERENCE: 4-30582A CURRENT PEPLICATION NUMBER: US/09/568,472 CURRENT FILING DATE: 1999-06-17 PRIOR APPLICATION NUMBER: 09/335,409 PRIOR FILING DATE: 1999-06-17 NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1 LENGTH: 68750 TYPE: DNA CREMISM: Sorangium cellulosum US-09-568-472-1	Alignment Scores: Pred. No.: Score: Score: 165.00 Matches: Percent Similarity: 15.74 Conservative: 17 Best Local Similarity: 28.74 Mismatches: 105.00 Matches: 70 Best Local Similarity: 28.74 Mismatches: 105 Chery Match: 3 Gaps: B: US-09-989-890-238 (1-212) x US-09-568-472-1 (1-68750) Qy 2 ProHisGlnAlaAlaAlaAlaAproValAspGlnThrProArgThrLeuAlaThrMetGlyGln 21
Qy 149 MetArgThrProAlaahla	SULT 1 SQUED Sequen Sequen SENERA APPLI AP	US-09-568-486-1 Alignment Scores: 71.6 Length: 68750 Score: 165.00 Matches: 70 Score: Percent Similarity: 28.7% Conservative: 17 Best Local Similarity: 28.7% Mismatches: 105 Query Match: 3 Gaps: 6 Conservative: 17 Best Local Similarity: 28.7% Mismatches: 105 Duery Match: 3 Gaps: 6 Conservative: 17 Mismatches: 105 Gaps: 8 Conservative: 17 Mismatches: 105 Mismatches: 105 Gaps: 8 Conservative: 17 Mismatches: 105 Mism	Oy 22 ArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProProAlaAla 41 23624TGAACGCGTCTGGTCGAGCAACAACGACTCGGCGCTCCCGCCTCCGCCCACATCA 23568 Qy 42CysSerGlyAspProGlyCysGlySerGlyAla

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ArgalaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProProAlaAla
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APPLICANT: Molnar, Istvan
APPLICANT: Molnar, Istvan
APPLICANT: 21rkle, Ross
APPLICANT: 21rkle, Ross
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT APPLICATION NUMBER: 09/335,409
PRIOR PILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
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US-09-567-899-1/C
; Sequence 1, Application US/09567899
; Patent No. 6383787
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
: APPLICANT: Ligon, James
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; ORGANIEM: Sorangium cellulosum
US-09-567-899-1
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SEQ ID NO 1
LENGTH: 68750
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Job time : 410 secs
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                                                                                   Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
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Command line parameters:
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-DB=Published Applications NA Main -QFWT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1_-LOOPCI=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-WATRIX_BAD10sumGs - TRANS=humanah 0.cdi -LIST=45 -DOCALIGGN=200 -THR SCORE=pct
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-WER-BOSSOSSOSSOS GCCN 1. 11026 Grunat 16032006 095522 16710 -NCPU=6 -ICPU=3
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-WARN IIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Sequence 799, App
Sequence 124, App
Sequence 56, Appl
Sequence 117, App
Sequence 12051, A
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(without alignments)
2247.575 Million cell updates/sec
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-989-920-56
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178.5
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Perfect score:
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RESULT 1

US-09-980-890-105

US-09-980-890-105

Sequence 105, Application US/0998980

PUBLICANT No. US20040166105A1

GENERAL INFORMATION:

APPLICANT: Salceda, Susana

APPLICANT: Macina, Roberto

APPLICANT: Bail, Chenghua

APPLICANT: Sul, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PrintING NATE: 2001-11-21

TITLE OF INVENTION NUMBER: US/09/989,890

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICANTION NUMBER: 60/252,509

FRIOR PLANTE OF SUL OF SUL
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US-IU-0/4-475-124

; Sequence 124, Application US/10074475
; Publication No. US20030092898A1
; CENERAL INFORMATION:
; APPLICANT: Saleeda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Karra, Kalpana
; APPLICANT: Carra, Kalpana
; APPLICANT: Cannoning
; APPLICANT: General Cannoning
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Genes and Proteins
; TITLE OF INVENTION: Genes and Proteins
; TITLE OF INVENTION: Cannoning
; FILE REFERENCE: DEX-0313
; CURRENT APPLICATION NUMBER: US/10/074,475
; CURRENT APPLICATION NUMBER: C0/268,292
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 295
; SEQ ID NO 124
; LENGTH: 654
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                                                                          SerProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly
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                                             US-09-989-890-238 (1-212) x US-10-104-047-799 (1-1785)
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                Gaps:
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US-10-074-475-124
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GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: No. US20030236392A1e1 full length cDNA
FILE REPRENENCE: H1-A0105;
CURRENT APPLICATION NUMBER:
PRIOR PELLICATION NUMBER:
PRIOR PELLICATION NUMBER:
SOUTHWARE: PATENTION DATE:
NUMBER OF SEQ ID NOS: 4096;
SOUTHWARE: PatentIn Ver. 2.1
SEQ ID NO 799
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Mismatches:
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CORGANISM: Homo sapiens
US-10-104-047-799
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US-10-104-047-799
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206
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 117, Application US/0998920;
Patent No. US20020172957A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Gen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-920-56
                                                                                                           4.51e-69
1002.50
94.5%
93.6%
                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                 Alignment Scores:
Pred. No.:
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Patent No. US20020172957A1

GENERAL INFORMATION:

APPLICANT: Recipon, Herve

APPLICANT: Chen, Sei-Yu

APPLICANT: Liu, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and F

FILE REPERENCE: DEX-0291

CURRENT APPLICANT: 120, Chenghua

TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and E

FILE REPERENCE: DEX-0291

CURRENT APPLICATION NUMBER: 08/09/989,920

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 60/252,500
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Matches:
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                                                1.95e-74
1065.50
95.8%
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  TYPE: DNA
ORGANISM: Homo sapien
                                                                Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
              ; ORGANISM: Hom
US-10-074-475-124
                                            Alignment Scores:
Pred. No.:
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US-09-989-920-56
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Percent Similarity:
Best Local Similarity:
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TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and PILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SEQ ID NO 117
LENGTH: 1977
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US-10-779-543-12051
Sequence 12051, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
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US-09-989-920-117
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APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: 10 CANGEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT APPLICATION NUMBER: US/10/779,543
PRIOR APPLICATION NUMBER: 09/217,471
PRIOR APPLICATION NUMBER: 09/217,471
PRIOR APPLICATION NUMBER: 06/068,755
PRIOR FILING DATE: 1998-12-23
PRIOR PELING DATE: 1998-12-23
PRIOR PELING DATE: 1998-04-03
PRIOR PELING DATE: 1998-04-03
PRIOR PELING DATE: 1998-00-04-10
PRIOR APPLICATION NUMBER: 60/080,664
PRIOR PELING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/012,910
PRIOR PELING DATE: 1999-01-28
PRIOR PELING DATE: 1999-01-28
PRIOR PELING DATE: 1999-01-28
PRIOR PELING DATE: 1998-02-24
PRIOR PELING DATE: 1998-02-24
PRIOR PELING DATE: 1998-03-31
PRIOR PELING DATE: 1998-03-31
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US-10-156-761-1440
'S-20-ence 1440, Application US/10156761
'Publication No. US20030119018A1
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US-10-779-543-12051
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                                                            ---ThralaCysProAlaProLeuProValValLeuValAlaProArgSerThrIleLeu 184
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APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADANOSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TITLE REPRENCE: 249-262
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
SEQ ID NO 1
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1529 TCATGGGCATCCGCGTCGACGAGT 1552
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ORGANISM: Streptomyces avermitilis
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Publication No. US20030119018A1
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; OTHER INFORMATION: a, t, c,
US-10-156-761-1
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Matches:
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                                                                                                           APPLICANT: SHIRM, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLB OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1440
LENGTH: 2034
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US-10-156-761-1440
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LOCATION: (1)
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) Publication No. US20030119018A1
) GENERAL INFORMATION:
) APPLICANT: OWURA, SATOSHI
) APPLICANT: IKEDA, HARUO
) APPLICANT: ISHIKAMA, JUN
) APPLICANT: ISHIKAMA, JUN
) APPLICANT: SHIBA, TADAYOSHI
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) APPLICANT: SHEM, TADAYOSHI
) APPLICANT: SHEM, TADAYOSHI
) APPLICANT: SHEM, TADAYOSHI
) APPLICANT: SAKAKI, YOSHIVKI
) APPLICANT: APTORI, WASAHIRA
) TILLE OP INVERTION: NOVEL POLYNUCLEOTIDES
) FILE REFERENCE: 249-262
) CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILLING DATE: 2002-05-29
) PRIOR FILING DATE: 2001-05-30
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                                                                                            1788289 GCCACCTGGGAAGGGAGTTTGAGCTCCTCGGCGACACCCCGGTCGGCGCCCGCACCCCCG
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APPLICANT: SHIBUYA, K.
APPLICANT: SHIBUYA, K.
APPLICANT: SHIBUYA, K.
TITLE CANT: SHIMIZU, N.
TITLE OF LINENTION: Novel hair keratin-associated proteins
FILE REPERENCE: 671304-2000
CURRENT APPLICATION NUMBER: 0204-05-13
CURRENT APPLICATION NUMBER: PCT/JP02/11851
PRIOR FILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO S.
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US-10-846-374B-5
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ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE REPREBNCE: 249-262
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
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ORGANISM: Streptomyces avermitilis
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                                                                              1334 AGCACCGTGTCTCCGTGC 1351
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Matches:
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Indels:
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6900
LENGTH: 1620
                                                                                                                                                                              TYPE: DNA ORGANISM: Streptomyces avermitilis
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Publication No. US20040005560A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560A1
FILE REPERENCE: H1-A0106
CURRENT PAPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1885
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US-10-108-260A-1885/c
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| Sequence 2.7, Application US/10483159 |
| Sublication No. US2005033042A1 |
| GENERAL INFORMATION |
| APPLICANT: Sabina, Belli |
| APPLICANT: Wallach, Michael |
| TITLE OF INVENTION: Nucleic Acids Encoding Recombinant 56 and 82 |
| TITLE OF INVENTION: Qemetocytes of Eimeria Maxima and Their Uses |
| FILE REFERENCE: 65175-A-PCT
                                                                                        SerGlySerSerGlnProTrpAlaAlaAlaSerAlaThrProMetLeuSer
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CURRENT FILING DATE: 2004-01-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
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ORGANISM: Chicken
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Percent Similarity: 36.0% Conservative: 14 Best Local Similarity: 29.8% Mismatches: 56 Query Match: 14.6% Indels: 90 DB: 5 Gaps: 12 US-09-989-890-238 (1-212) x US-10-097-340-42 (1-5142)	Qy 19 MetGlyGlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeu 35	Qy 36 SerProProProAlaAlaCysSerGly	48 CysGlySerGlyAlaGlyLeuPro	Db 1886 TGTTCTTCTGGAACATACTCTGCCATGTCTCTCTCTGAAGTCTCCTCCAGGTCCC 1827 Qy 56 SerAlaSerAlaAlaGly1leAlaSerSerAlaValGluPro70 Dh 1826 TGTTCTCTCCAGGTCTCC 1827	71ValCysGlyAspAlaAlaProAlaCysLeuLeuArgThrProLeu 	Oy 86 ArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCysProProAlaLeuIle 105	Qy 106 ValHisProProAlaGlyGlyMetAlaSerGlySerSerGlnProTrpAla 122	Qy 123 AlaAlaSerAlaThrProMetLeuSerSerLyBAlaSerLeuCyBIleProThrArgGly 142	Qy 143 ProProGinProLeuMetArgThrProAlaAlaArgSerHisTrpProIleProHis 162	Qy 163 ProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArgSerThr 182 Db 1562	183 -IleLeuSerMetSerArgThr-TrpThrCysArgArgT 	Qy 195 rpAlaValAlaProCysArg 201	RESULT 15 US-11-050-926-42/c ; Sequence 42, Application US/11050926 ; Publication No. U320050214831A1	; APPLICANT: JOHN MONAHAN ; APPLICANT: Manjula GANNAVARAPU ; APPLICANT: Sebastian HOERSCH ; APPLICANT: Shubhangi KAMATKAR	APPLICANT: STEWN G. KOVATS APPLICANT: Rachel B. MEYERG APPLICANT: Michael MORRISEY APPLICANT: Peter OLANDT APPLICANT: Peter OLANDT APPLICANT: Peter OLANDT APPLICANT APPLI	; APPLICANT: Ami SEN ; APPLICANT: Peter VEIBY ; APPLICANT: Gordon B. MILLS ; APPLICANT: Robert C. BAST, Jr. ; APPLICANT: Karen LU
1218 GCATCTTCTCCTCCTGCTCCCGCATCTTCTCCTCCTGGCCCCCGCATCTTC 90 sProThrGlyProArgSerThrMetGluCysProProAlaLeuIleValHisProProAl	110 AGLYGIYMeTALASGETSJYSGETSGETGINFOTTPALAALAAATHEPFOMETLE 1107 ATCTCCTCCTGCCCCGCATCTTCTCCTCCTGGCCCCGCATCTTCTCCTCCTCTTCTTCTTCTTTTTTTT	<pre>dy</pre>	Qy 150 rgThrProAlaAlaArgSerHisTrpProIleProHisProCysAspThrA 167	Oy 167 laCysPro-AlaProLeuProValValLeuValAlaProArgSerThrIleLeu 184	RESULT 14 US-10-097-340-42/c ; Sequence 42, Application US/10097340 ; Publication No. US20030087250A1	; GENERAL INCRMATION: ; APPLICANT: John MONAHAN ; APPLICANT: Manjula GANNAVARAPU ; APPLICANT: Sebastian HOERSCH	; AFFLICANT: SNUDDRNG KAWATKAK ; APFLICANT: Rachel E. MEYERS ; APFLICANT: Rachel E. MEYERS ; APFLICANT: Michael MORRISEY	; APPLICANT: Peter OLANDT ; APPLICANT: Ami SEN ; APPLICANT: Peter VEIBY ; APPLICANT: Gordon B. MILLS	; APPLICANT: ROBET C. BAST, Jr. ; APPLICANT: Resemante SCHMANDT ; APPLICANT: Rosemante SCHMANDT ; APPLICANT: Xumei ZHAO	 APPLICANT: NAZEH GLATT TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: ASSESSMENT, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030 	CURRENT APPLICATION NUMBER: US/10/097,340 ; CURRENT FILING DATE: 2002-03-14 ; PRIOR PPLLICATION NUMBER: 60/276,025 ; PRIOR FILING DATE: 2001-03-14	PRIOR APPLICATION NUMBER: 60/325,149	; PRIOR APPLICATION NUMBER: 80/324,56/ ; PRIOR APPLICATION NUMBER: 60/311,732 ; PRIOR FILING DATE: 2001-08-10 ; PRIOR APPLICATION NUMBER: 60/325,102	PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19 NUMBER OF SEQ ID NOS: 363 SOFTWARE: PastSEQ for Windows Version 4.0	; SEQ ID NO 42 ; IENGTH: 5142 ; TYPE: DNA ; ORGANISM: Homo sapiens	US-IU-09/-340-42 Alignment Scores: 0.00269 Length: 5142 Pred. No.: 166.00 Matches: 68

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Search completed: March 17, 2006, 07:16:30 Job time : 4711 secs
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APPLICANT: Rosemarie SCHWANDT
APPLICANT: Xumel ZHAO
APPLICANT: Xumel ZHAO
APPLICANT: Xtaren GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins Por The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/11/050,926
CURRENT APPLICATION NUMBER: US/10/097,340
FRIOR PAPLICATION NUMBER: 60/276,025
FRIOR FILING DATE: 2001-03-14
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FRIOR APPLICATION NUMBER: 60/324,967
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ORGANISM: Homo sapiens
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Sequence 162, App Sequence 36, Appl Sequence 3025, App Sequence 745, App Sequence 745, App Sequence 21912, A Sequence 21912, A Sequence 12594, A Sequence 12594, A Sequence 12181, A Sequence 12181, A Sequence 12181, A Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 54, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 18205, A

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Scoring table:

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8 US-10-858-730-162

8 US-10-858-730-162

1 US-11-136-52-3025

7 US-11-128-061-745

1 US-11-128-061-745

9 US-11-096-568A-21912

9 US-11-096-568A-19912

9 US-11-096-568A-12912

9 US-11-096-568A-12912

9 US-11-096-568A-12912

12 US-11-1006-568A-12912

13 US-11-1006-568A-12912

14 US-11-1006-568A-1291

15 US-11-1006-568A-1291

16 US-11-096-568A-1291

17 US-11-1096-568A-1291

18 US-11-052-554A-54

19 US-11-096-568A-1559

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16 US-11-096-568A-1559

17 US-11-096-568A-1559

18 US-11-075-198-58

18 US-11-075-198-58

18 US-11-075-169-35

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18 US-11-114-798-39

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APPLICANT: MASUHO, YASUHIKO
TITLE OP INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/11/072,512 CURRENT FILING DATE: 2005-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/350,978
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; Sequence 799, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISHLI, SHIZUKO
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ISONO, YUUKO
HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
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OTSUKI, TETSUJI
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-MODEL=frame+_p2n.model -DEV=xlh
-O=/abss/ABSGWEB spool/US0999890/runat_16032006_095254_16764/app_query.fasta_1
-O=/abss/ABSGWEB spool/US09998990/runat_16032006_095254_16764/app_query.fasta_1
-DB=Published_App_ications_NA_New -QFWT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.T_-LCOPCL=0 -LCOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL_OUTPWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0-MAX_EEN=2000000000 -HOST=abss03h
-MAX_EEN=2000000000 -HOST=abss03h
-USBR=US09989990 @CCN 1 1 431 @runat 16032006_095254_16764 -NCPU=6 -ICPU=3 -NORMAP -NG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DBY INMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XCAPEXT=0.5 -FGAPDP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 9547, Ap
Sequence 306, App
Sequence 16769, A
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1: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB. seq:*

2: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB. seq:*

3: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB. seq:*

4: /cgn2 6/ptodata/1/pubpna/USO7 NEW PUB. seq:*

5: /cgn2 6/ptodata/1/pubpna/USO9 NEW PUB. seq:*

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9: /cgn2 6/ptodata/1/pubpna/USO1 NEW PUB. seq:*

10: /cgn2 6/ptodata/1/pubpna/USO1 NEW PUB. seq:*

11: /cgn2 6/ptodata/1/pubpna/USO1 NEW PUB. seq:*

12: /cgn2 6/ptodata/1/pubpna/USO1 NEW PUB. seq:*

13: /cgn2 6/ptodata/1/pubpna/USO1 NEW PUB. seq:*
                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                          nucleic search, using frame_plus_p2n model
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Fgapop 6.0 , Fgapext
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Database :

Score

Result

1128 163.5 162.5 162

Sequence 44656, A Sequence 1558, A Sequence 15585, A Sequence 475, App Sequence 1019, App Sequence 550, App Sequence 550, App Sequence 352, App Sequence 352, App Sequence 2, App Sequence 8975, App Sequence

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247 GICTGGGACCICACCAACCCGGTGCGTCGTCGGCGACGGCACCGTCGGCACCGACTAC 306
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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| NAME/KEY: misc_feature
| LOCATION: (1)._(1306)
| OTHER INFORMATION: Ceres Seq. ID no. 12613953
| US-11-096-568A-9547
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FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 9547
LENGTH: 1306
LENGTH: 1306
TYPE: DNA
ORGANISM: Triticum aestivum
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US-11-096-568A-9547
US-11-096-568A-9547, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Abaxandrov, Nickolai et al.
ITILE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
ITILE OF INVENTION: Therby
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                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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Gaps:
                  2001-379298
 PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 200;
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 799
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1128.00
99.5%
99.5%
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                                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-11-072-512-799
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Best Local Similarity:
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Pred. No.:
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ORGANISM: Zea mays subsp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7033 GGATGCTCTTCTGGTGGTCGGTCTCCTCGAGCTGCAGCCTCAGCGTGGTCAGCTCCTGCT 6974
                                                        Sequence 306, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Myeth

APPLICANT: Myeth

TITLE OF INVERTION: Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVERTION: Probe 301896-041000 (AM101086)

CURRENT FILING DATE: 2005-05-25

CURRENT FILING DATE: 2005-05-25

FRIOR PILING DATE: 2005-05-36

NUMBER OF SEQ ID NOS: 362830

SEQ ID NO 306

LENGTH: 15234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 MetGluCysProPro------AlaLeuIleValHisProProAlaGly 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 SerSerLysAlaSerLeu-----CysIleProThrArgGlyProProProGln----- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 SerleuAlaLeuLeuSerArgProLeuSerProProProAlaAlaCysSerGlyAspPro 46
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Mismatches:
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Matches:
--TCATCCATGCGCTCT 883
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; ORGANISM: Rattus norvegicus
US-11-136-527-306
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby TITLE REFERENCE: 2750-1592P025 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT APPLICATION NUMBER: US/11/096,568A NUMBER OF SEQ ID NOS: 34471 SEQ ID NOS: 34471 SEQ ID NOS: 34471 LOSS LENGTH: 2052
                                                                                                           6568 CCGCCTGCAGCCGTTTCTGGGCAGCCT---CCTGGGCCAGCTGCAGCTGCCTCGCAGACT 6512
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---ProAlaAlaArgSerHisTrpProIleProHisProCysAspThrAlaCysProAla 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 ------ThrTrpThrCysArgArgTrpAlaValAlaProCysArgAlaGluL 204
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Matches:
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US-11-096-568A-16769
; Sequence 16769, Application US/11096568A
; Publication No. US20660048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
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40 AlaAlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeu	4111 TCAGGGGGGAATGGCCCCGGCCTGGGCCTGCTGCTGGTGCCGGTTGCTTTG 4052 4051 AAGACGCGCTTGGGCTCTGAACATCCAGGTGGAGCGGCTGGCCCCGGCT 3992 4051 CAACACCGCCTTGGGCTCTGAACATCCAGGTGGAGGGGCGCTGGCCCCGGCT 3992 Qy 162 HisProCysAspThrAlaCysProAlaProLeuProAlAlaProArgSc 181	RESULT 6 US-11-186-731-4/C is Gequence 4, Application US/11186731 sequence 4, Application No. US2005025521A1 sequence 4, Application No. US2005025521A1 GENERAL INFORMATION: APPLICANT: Repeller-Libermann, Rosana TITLE OF INVENTION: S9079 and 12599, Protein Kinase Family TITLE OF INVENTION: Members and Uses Therefor FILE REFERENCE: MP12001-047P1RCP1 (No. CURRENT APPLICATION NUMBER: US/11/186,731 CURRENT APPLICATION NUMBER: US/11/186,731 PRIOR FILING DATE: 2005-07-21 PRIOR PELING DATE: 2001-02-15 NUMBER OF SEQ ID NOS: 9 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 24120 TYPE: DNA CORGANISM: HOMO SapienS FRAIURE: RAANCKEY: 5.UTR
114 AlaSerGlySerSerGlnPrOTrpAlaAlaAlaSerAlaThr	INI INI INI INI INI INI INI INI INI INI	NUMBER OF SEC 1D NOS: 9 NUMBER OF SEC 1D NOS: 9

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APPLICANT: Truchedary, Joshua
APPLICANT: Truchedary, Michael J.
APPLICANT: Yorgey, Peter S.
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
ITILE OF INVENTION: PRODUCTION
ITILE OF INVENTION: PRODUCTION
CURRENT APPLICATION NUMBER: US/10/858,730
CURRENT FILING DATE: 2004-06-01
FRIOR PAPLICATION NUMBER: US 60/475,000
FRIOR FILING DATE: 2004-06-01
FRIOR PILING DATE: 2004-06-03
FRIOR PILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOPTWARE: FASTERO FOR WINDOWS Version 4.0
SEQ ID NO 162
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Matches:
Conservative:
Mismatches:
Indels:
 3951 CCTTGTACCACGTCACCTCTG 3931
                                         US-10-858-730-162
; Sequence 162, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptomyces coelicolor
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                                                                                                                                                    Driggers, Edward M.
Madden, Kevin T.
                                                                                                                                                                                O'Leary, Jessica
O'Toole, George
                                                                                                     APPLICANT: Bailey, Richard | APPLICANT: Blomquist, Paul
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Best Local Similarity:
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Conservative:
Mismatches:
Indels:
Gaps:
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; LOCATION: (23979)...(24120)
US-11-186-731-4
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                           NAME/KEY: CDS
LOCATION: (72)...(23978)
FEATURE:
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LOCATION: (1) ... (71)
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Query Match:
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APPLICANT: Woeth
APPLICANT: Wouts, William M
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APPLICANT: Wouts, William M
APPLICATION: DATE: 2008-04:006
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE PATENTIN VETRION 3.2
SEQ ID NO 3025
LENGTH: 3334
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--AlaSerLeuCysIlePro
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GREAKAL INFORMATION:

APPLICANT: Balley, Faul

APPLICANT: Diggers, Edward

APPLICANT: Driggers, Edward M.

APPLICANT: Driggers, Edward M.

APPLICANT: Driggers, Edward M.

APPLICANT: O'Toels, George

APPLICANT: O'Toels, George

APPLICANT: Trucheart, Joshua

APPLICANT: Walbridge, Michael J.

APPLICANT: Walbridge, Michael J.

APPLICANT: Walbridge, Michael J.

TITLE OF INVENTION: BETOUCTION

TITLE OF INVENTION: PRODUCTION

TITLE OF INVENTION: WUMBER: US/10/858,730

CURRENT APPLICATION NUMBER: US 60/475,000

PRIOR FILING DATE: 2004-06-01

PRIOR FILING DATE: 2004-06-01

PRIOR FILING DATE: 2004-03-10

MUMBER OF SEQ ID NOS: 364

SEQ ID NO 36

LENGTH. 2625

TURNED: DATE

LENGTH. 2625
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
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Methods in Cancer
TITLE OF INVENTION: Novel Compositions and PILE REFERENCE: 529452001300 CURRENT APPLICATION NUMBER: US/10/330,773 CURRENT FILING DATE: 2002-12-27 NUMBER OF SEQ ID NOS: 981 SOFTWARE: FREUSEQ FOR Windows Version 4.0 SEQ ID NO 278 LENGTH: 127722
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; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
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                                                                                                                                                                        ; LOCATION: (1)...(127722)
; OTHER INFORMATION: n = A,T,C or
US-10-330-773-278
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156.50
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                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AlaAlaGlyIleAlaSerSerAlaVal------GluProValCysGlyAspAlaAla 76
                                                                                                                                                                                                                                                            22 ArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAlaAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ProProAlaGlyGlyMetAlaSer---GlySer---
                                                                                                                                                                                                                                                                                                                  42 CysSerGlyAspProGlyCys-----GlySerGlyAlaGlyLeuProSerAlaSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                    77 ProAlaCysLeuLeuArgThrProLeuArgGlyLeuLeu-----LysProThrGly
                                                                                                                                                                                                                                 US-09-989-890-238 (1-212) x US-11-136-527-3025 (1-3334)
                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
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    TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                              27.1
157.00
36.2%
30.6%
13.8%
                                                         ; OTHER INFORMATION: n is a, US-11-136-527-3025
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                             FEATURE:
NAME/KEY: misc feature
LOCATION: (690)..(690)
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Best Local Similarity:
Query Match:
DB:
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US-10-330-773-278/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 rSerAlaValGlu---ProValCysGlyAspAlaAlaProAlaCysLeuLeuArgThrPr 84
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127722
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                                                   Conservative:
Mismatches:
Indels:
         Length:
Matches:
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APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
APPLICANT: Mounts, William M.
APPLICANT: Sinacore, Martin S.
APPLICANT: Sinacore, Martin S.
APPLICANT: Brown, Buggene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: MAKING AND USING SAME
TITLE OF INVENTION: MAKING AND USING SAME
TITLE OF INVENTION: WAKING AND USING SAME
TITLE OF INVENTION NUMBER: US/11/128,049
CURRENT APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2005-05-11
NUMBER OF SEQ ID NOS: 7285
SOOTWARE: Patentin version 3.3
SOOTWARE: Patentin version 3.3
FROM PATENTIAL NO 74519
                                                                                                                                    3352 TCAGCGTCGTCGTCCTGCTCCACCTGGGCCTTCTGCCGCAGCGTCTGCTCTGCAAACT 6293
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6145 CCTCCGCCGACTGTTTCAGCCGCTCCGCCTCTT------CCACTTGTTTCC 6101
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                                         71 ValCysGlyAspAlaAlaProAlaCysLeuLeuArgThrProLeuArgGlyLeuLeuLys 90
                                                                                                             91 ProThrGlyProArgSerThrMetGluCysProProAlaLeuIleValHisProProAla
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Publication No. US20060010513A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Charlebois, Timothy S.
APPLICANT: Mounts, William M.
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LOCATION: (5981)..(5999)
OTHER INFORMATION: n is a, c, g,
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APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
FILE REFERENCE: 01997.027701
CURRENT APPLICATION NUMBER: US/11/128,061
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
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SOFTWARE: Patentin version 3.3
SEQ ID NO 745
LENGTH: 14619
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155.50
39.7%
28.8%
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LOCATION: (2751)..(2765)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (14598)..(14619)
OTHER INFORMATION: n is a,
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NAME/KEY: misc_feature
LOCATION: (5981)..(5999)
OTHER INFORMATION: n is a,
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INFORMATION: n is a,
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LOCATION: (9420)..(9510)
OTHER INFORMATION: n is a,
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LOCATION: (12124)..(12151)
OTHER INFORMATION: n is a,
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LOCATION: (13563)..(13585)
OTHER INFORMATION: n is a,
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LOCATION: (7283)..(7317)
OTHER INFORMATION: n is a,
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LOCATION: (7320)..(7334)
OTHER INFORMATION: n is a,
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LOCATION: (6573)..(659
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Best Local Similarity:
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DB:
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Sequence 23836, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT PILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                      1543 CTA------GAACCAGCGCACCACCACCGCTCCGCCATGGGCACGCCTGGGCACA 1496
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                                    167 AlaCysProAlaProLeuProValValLeuVal-----AlaProArgSerThrile 183
                                                                                                   184 LeuSerMetSerArgThrTrpThrCysArgArgTrpAlaValAlaProCysArgAlaGlu 203
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5980 TCTGCTGCAGCTCCTCTTCCCGCTGCTGCACAAAGGCATGCGCCTTC-TCCTCT---
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; OTHER INFORMATION: Ceres Seq. ID no. 12415689
US-11-096-568A-23836
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ORGANISM: Zea mays subsp. mays
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NAME/KEY: misc feature
LOCATION: (7283)..(7317)
OTHER INFORMATION: n is a,
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LOCATION: (12124)..(12151)
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LOCATION: (13563)..(13585)
OTHER INFORMATION: n is a,
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LOCATION: (6573)..(6594)
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Sequence 19912, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Abexandrow, Nickolai et al.

ITILE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TITLE OF INVENTION: Therby

FILE REFERENCE: 2790-19522P02

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 19912
110
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                                                                                                                                                                                                                                                                                                       -----AlaValAlaProCysArgAl 202
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                                                                                  118 rGlnProTrp----AlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLe
sProThrGlyProArgSerThrMetGluCysProProAlaLeuIleValHisProProAl
                                                        -GlyGlyMetAlaSerGlySerSe
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Matches:
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; OTHER INFORMATION: Ceres Seq. ID no. 12375592
US-11-096-568A-19912
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ORGANISM: Zea mays subsp. mays
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US-11-096-568A-19912
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REPERBNCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT APPLICATION NUMBER: US/11/096,568A
KUMBER OF SEQ ID NOS: 34471
SEQ ID NO 21912
LENGTH: 1269
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Conservative:
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                                                                          GlnProLeuMetArgThrProAla----
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OTHER INFORMATION: Ceres Seq. ID
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ORGANISM: Zea mays subsp. mays
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US-11-096-568A-21912
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Pred. No.:
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-OUTFWT=pto -NORM=SXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=ABS803h
-USER=US0998980 @CGN 1 1 493 @runat 16032006_095515_17514 -NCPU=6 -ICPU=3
-NO WMAP -NGG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
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                                                                                Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
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humanexons or transcripts, for detecting expression and other uses
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PR Corporation (NY) (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                   Salceda,S., Macina,R.A., Recipon,H., Pluta,J., Sun,Y. and Liu,C. Compositions and methods relating to breast specific genes and
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                                                                                                                                                Patent: WO 02077232-A 105 03-OCT-2002;
Diadexus, Inc. (US)
Location/Qualifiers
1. 1713
/organism="Homo sapiens"
/nol_type="unassigned DNA"
/db_xref="taxon:9606"
Sequence 105 from Patent WO02077232. AX644347.1 GI:28610406
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212
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquirtes: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Jun 17, 2002 this sequence version replaced gi:20218554.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/c_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chri
RP11-344H11 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                    AL356390 bNA linear PRI 18-MAY-2005
Human DNA sequence from clone RP11-344H11 on chromosome I Contains
the NROB2 gene for nuclear receptor subfamily 0 (group B, member
2), the S' end of a novel gene (FLL12455), the NUDC gene fornuclear
distribution gene C homolog (A. nidulans), a novel gene (FLJ34633),
a ribosomal protein L12 (RPL12) pseudogene, a novel gene (FLJ34633),
two Opg islands, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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/note="Sequence from overlapping clone RP4-633N17
(ALI37860). Assembly confirmed by restriction digest."
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Homo sapiens (human)
201 ArgalaGluLysLeuMetCysSerSerSerArgSer 212
                                704 CGAGCCGAGAAATTGATGTGCTCATCTTCAAGAAGC 739
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VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1402.7
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32162 AGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGC 82221
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Homo sapiens chromosome 1 clone RP3-426N7, 7 unordered pieces.
ALS92304
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                      LeuArgThrProLeuArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCys
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                                                                                 21 GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
                                                                                                           61 AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: betraminator Big Dye; 100% of reads
Consensus quality: 110287 bases at least Q40
Consensus quality: 110500 bases at least Q40
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Web site: http://www.sanger.ac.uk
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
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/ Joun tage="RP11-34H11.3"
/ Joun tage="
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GACVRGCSPCLSTEDSTEGTAEANWAKEHNGVPPSPDRAPPSRRDGQRLKSTMGSSPS
YPDVKLKGIPVYPYPRATSPAPDADSCCKEPLADPPPMRHSLPSTFASSPRGSEEYYS
PHESDLDLPEMGSGSMSSREIDVLIFKKLTELFSVHQIDELAKTSPTVFLEKTSKIS
DLISSITQDYHLDEQDAEGRLVRGIIRISTRKSRARPQTSEGRSTRAAPPAAPDSG
HETMVGSGLSQDELTVQISQETTADAIARKLRPYGAPGYPASHDSSFGTDTDSSGAP
LLQVYC"
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/locus tag="RP11-344H11.3-001"
complement join(87577. .88309,88753. .88871,88966. .89049,
91374. .91568,91663. .91779,92621. .92686,92779. .92982,
110273. .110350,112510. .112713)}
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complement(join(87577. .88309,88753. .88871,88966. .89049,
91374. .91568,91663. .91779,92621. .92686,92779. .92982,
110273. .110350,112510. .112713))
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match: cDNA6: Em:AK012321.1 Em:AL136725.1 Em:BC007280.1
Em:BC015153.1"
                                                                            Complement (join (53464. .53610,53925. .54274))
/locus tag="RP11-344H11.4-001"
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Tr:Q86ZX1 Tr:Q8AVWO Tr:Q8CZKO Tr:Q9OVV6 Tr:Q9NQ02"
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/codon_start=1
/product="novel protein"
/protein id="CALI1559.1"
/db_xref="GI:55959149"
/db_xref="UniProt/TrEMBU:Q5QP32"
                                                                                                                                                                                                                                               'codon_start=1
'product="ribosomal protein L12 (RPL12) pseudogene"
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/product="nuclear distribution gene C homolog
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standard_name="OTTHUMP00000004472"
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Matches:
Conservative:
Mismatches:
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/locus_tag="RP11-344H11.4-001"
/pseudo
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Best Local Similarity:
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US-09-989-890-238 (1-212) x AL356390 (1-140207)

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96128 CCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGGATGGCCAGCGGGCTCAAGTCAACC 96187
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Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                     AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
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                                                            GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
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Patent: BP 1308459-A 799 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
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/db_xref="taxon:9606"
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Consensus quality: 110681 bases at least Q20
Insert size: 111138; sum-of-contigs
Insert size: 119403; 8.4% error; agarose-fp
Quality coverage: 11.23x in Q20 bases; sum-of-contigs Quality
coverage: 10.67x in Q20 bases; agarose-fp
                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                   18958: contig of 18058 bp in length 1859 35144: contig of 16986 bp in length 1859 35144: gap of 100 bp 245 35244: gap of 100 bp 245 54710: contig of 19466 bp in length 1711 54810: gap of 100 bp 25810: contig of 18126 bp in length 17236: contig of 18126 bp in length 17236: contig of 1852 bp in length 1889 92888: gap of 100 bp 1889 92888: gap of 100 bp 1889 10873: contig of 15751 bp in length 1840 111738: contig of 2899 bp in length 1840 111738: contig of 2899 bp in length 1840 111738: contig of 2899 bp in length.
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/clone="RP3-426N7"
1. 18058
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fragment chain:1"
54811...72936
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73037...92888
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fragment_chain:2"
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Conservative:
Mismatches:
Indels:
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note="assembly_fragment:02454
ragment_chain:1"
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18159. .35144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPRPGHPRPASGPPRLGPWERPTELCLETYDKPPQPPPSRRTRR
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PHRSDLDLPEMGSGSMSSREIDVLIPKKLTELFSVHQIDELAKCTSDTVFLEKTSKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (G-JUL-2002) Taka 1:genomics@hri.co.jp, Tel:81-2438-52-3975, Fax:81-438-52-3986) Whistophy Chiba compared by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA full insert sequencing: Key Technology Center etc.); 5'- & 3'-end one pass sequencing: Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB; and stocknology Center, National Institute of Technology and Bralation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB;
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HETWYGSGLSQDELTVQISQETTADAIARKLRPYGAPGYPASHDSSFQGTDTDSSGAP
LLQVYC"
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         Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                  253 CAGAGAGCATTACCTTCATCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
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Homo sapiens cDNA FLJ34633 fis, clone KIDNE2015710.
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oligo capping; fis (full insert sequence).
Homo sapiens (numan)
Homo sapiens
                                    Conservative:
Mismatches:
Indels:
         Matches:
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                                 Percent Similarity:
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macina, R.A., Recipon, H., Chen, S.Y., Sun, Y. and Liu, C. Compositions and methods relating to lung specific genes proteins
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Patent: WO 0102568-A 2132 11-JAN-2001;
CHIRON CORPORATION (US) ; HYSEQ, INC. (US)
Location/Qualifiers
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                               1. .427
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1. .427
/note="n = A,T,C or G"
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Sequence 56 from Patent WO02068633.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J., Kassam, A., Reinhard, C., Randazzo, F., Kennedy, G.C., Pot, D., Lanson, G., Dramac, R., Crkenjakov, R., Drwanac, S., Dickson, M., Labat, I., Leshkowitiz, D., Kita, D., Garcia, V. and Strache-Crain, B. Human genes and gene expression products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            493 CCCCCAGCCCTGATCGTGCACCCCCCAGCGGGGATGGCCAGCAG-CTCAAGTCAACC
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Sequence 2132 from Patent WO0102568.
AX071660.
AX071660.1 GI:12582011
                                                                          Gaps:
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Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentla;
Sciurognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 1680)
Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschult, S.F., Zeeberg, B., Butch, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Mooret, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Banddo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 16 Row: p Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 19526881. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (27-APK-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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Contact: MGC help desk
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                                                                                                                  357 AGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGC 416
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Diadexus, Inc. (US)
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                                     US-09-989-890-238 (1-212) x AX535029 (1-1977)
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BC006890.1 GI:13905189
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BC006890
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/db_xref="d1:13905190"
/db_xxef="denelD:69073"
/db_xxef="denelD:69073"
/db_xxef="Wd1:1316323"
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ASGAPAPGYTGTGTGLE98ARAAG1ACSPSFNGTWCTAAAPAPATLEPTPLKGTFFPREWTY
VCPPARTVHPPAAGMKGSRPAMAAASATLMLSSKASLSTPTAMPPPGSLTWTPAARS
PWPSLLIPHGTACLAPSPTAPAALRSSTTPSMNTWTCLRWAVAPCRAGRSTCLFSRS"
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 68130)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Homo sapiens PAC clone RP5-1098J4 from 7, complete sequence.
ACO04961
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Center code: WUGSC
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Mismatches:
Indels:
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Contact: sapiens@watson.wustl.edu
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Center project name: H_DJ1098J04
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clone.

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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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The clone sequenced to the right is RP5-88608, 200 bp overlap.
Actual start of this clone is at base position 1 of RP5-1098J4, actual end is at 57367 of RP5-88608.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one male donor.

The clone may be obtained either from Genome Systems, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match to EST AA330816 (NID:g1983079)"
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(http://www.resgen.com); or from Pieter de Jong.
VECTOR: pCYPAC2
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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245. 463
/rpt_family="Mariner"
474. 665
/rpt_family="Ll"
673. 040
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/clone_lib="RPCI-5"
1. .244
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5482. .5757
/rpt_family="L1"
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4049. .4432
/rpt_family="MaLR"
4650. .4749
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876. .4911
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6301_ .6609
/rpt_family="Alu"
6757 . .6809
/rpt_family="L1"
6810_ .6951
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/rpt_family="L1"
3719. .400
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6133. for
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AC147052 170236 bp DNA linear PRI 03-JAN-2004
Pan troglodytes BAC clone RP43-143G1 from 7, complete sequence.
AC147052 GI:40018813
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Submitted (03-JAN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Dec 18, 2003 this sequence version replaced gi:38154079.
                    /rpt_family="MER2_type"
22945. .23020
/note="similar to Mus musculus EST AA619820 (NID:g2523696)
v161c07:s1"
22945. .23020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (chimpanzee)
Pan troglodytes
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 17023)
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Direct Submission
Submitted (18-DEC-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 170236)
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Center code: WUGSC
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1 (bases 1 to 170236)

1 Levy, A., Kozlowicz, A. and Haglund, K.
The sequence of Pan troglodytes BAC clone RP43-143G1
Unpublished (2001)

2 (bases 1 to 170236)
Wilson, R.
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Conservative:
Mismatches:
Indels:
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Unpublished (2001)
3 (bases 1 to 170236)
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6560. .16686
.rpt_family="Alu"
7300. .17389
inote="similar to Mus musculus EST AA619820 (NID:g2523696)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.610.07.81"
17302. .17398
/note="similar to Mus musculus EST AA655227 (NID:g2591381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus EST AA655227 (NID:92591381)
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Anote="aimilar to Mus musculus EST W09437 (NID:g1283754)
ma63a04.rl"
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                                                                                                                                                                                                                                                                                                                     794. .9911
note="match to EST AA330816 (NID:g1983079)"
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21318. .22078
22155. .22519
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22155. .22519
/rpt_family="MBR2_type"
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11013. .11126
/rpt_family="L2"
12991. .13231
/rpt_family="WIR"
13813. .13918
/note="similar to Mus m
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19157. 19273
1974. 19373
/rpt_family="Alu"
19774. 19303
/rpt_family="Ar_rich"
19341. 19756
/rpt_family="L1"
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/rpt_family="Alu"
20728. .20942
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5561. .15797
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10992. .21034
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                                                                                                                                                            /rpt_family="Other" 6976. .7423 /rpt_family="MalR" 7446. .7693
                                                   /446. .7693
/rpt_family="L1"
7802. .8121
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8428. .8710
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4796. .14823
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4302. .14592
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The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0471; birthdates : 6-6-80). The clone and detailed information can be obtained from RedGen (http://www.resgen.com) or Pieter de Jong and co-workers at
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                                                                                                                                                             Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
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chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC146125.

    .40<sup>-</sup>
/note="Sequence derived from PCR product of project

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1 (bases 1 to 172424)
Griffin, M., Haglund, K. and Haakenson, W.
The sequence of Pan troglodytes BAC clone RP43-4K13
Unpublished (2001)
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.bacpac.chori.org.
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Sulston, J.E. and Wilson, R.
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                                                                                                                                                                                                                                     http://genome.wustl.edu
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Best Local Similarity:
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AC146125
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
TITLE
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The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, Clint', Yerkes #C0411; birthdate: 6-6-80). The clone and detailed information can be obtained from ResGen
                                                                                                                                                                                                                                                                                                                                                                                               USA
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Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this cone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                         03) Genetics, Genome Sequencing Center, 4444 St. Louis, MO 63108, USA
                                                                                                                                                                                                     Direct Submission
Submitted (03-SEP-2003) Genetics, Genome Sequencing Center, 4444
Porest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                               63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.resgen.com) or Pieter de Jong and co-workers at http://www.bacpac.chori.org.
                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-SEP-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Sep 3, 2003 this sequence version replaced g1:33387079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
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This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
------ Summary Statistics
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Conservative:
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Indels:
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|mol_type="genomic DNA"
|db_xref="taxon:9598"
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/clone_lib="RPCI-43"
Unpublished (2001)
3 (bases 1 to 172424)
Wilson,K.K.
Direct Submission
Submitted (01-AUG-2003) G6
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                                                                                                                            Forest Park Parkway, S
4 (bases 1 to 172424)
Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      code: WUGSC
                                                                                                                                                                                                                                                             Porest Park Parkway, S
(bases 1 to 172424)
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; Neisseria.

E (bases 1 to 525)

S Moe, G.R., Tan, S. and Granoff, D.M.

Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains

L Infect. Immun. (1999) In press

E (bases 1 to 525)

S Moe, G.R., Tan, S. and Granoff, D.M.

Direct Submission

L Submitted (04-AUG-1999) Children's Hospital Oakland Research

Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aci,ob/y 525 bp DNA linear BCT 06-SEP-1999
Neisseria meningitidis strain M136 surface protein A (nspA) gene,
API75679
                                                                                                               /trānslation="MKKALATLIALAI PAAALAEGASGFYVQADAAHAKASSSLGSAK
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ARLSINRASYDLGGSDSFSQTSTGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKN
VRSGELSAGVRVKF"
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1. .525
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Matches:
Conservative:
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Indels:
Gaps:
                                                            72277 CITCCAICCAGCCICGCICCTCCTGAGCCGCCCC 72309
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                                           24 LeuProSerSerLeuAlaLeuLeuSerArgPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 ProSerAlaSerAlaAlaAlaGlyIleAla 64
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/gene="nspA"
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Neisseria meningitidis

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Bacteria; Proteobacteria;

Roisseria meningitidis

B (bases 1 to 525)

Lofet. Immun. (1999) In press

Moc G.R., Tan, S. and Granoff, D.M.

Infect. Immun. (1999) In press

Moc G.R., Tan, S. and Granoff, D.M.

Lofet. Submission

Locet. Submission

Locet. Submission

Locet. Submission

Locet. Manual Street, Oakland, CA 94609, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKKALATLIALAIPAAAIAEGASGFYVQADAAHAKASSSIGSAK
GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLG
ARLSINRASVDLGGSDSFSQTSTGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKN
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Neisseria meningitidis strain NG3/88 surface protein A (nspA) gene,
complete cds.
                                                                                                                                        Neisserial Surface Protein A strains
SM Neisseria meningitidis

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

E 1 (bases 1 to 525)

S Moe, G.R., Tan, S. and Granoff, D.M.
Differences in Surface Expression of Neisserial Surface Protein is among Neisseria meningitidis Group B strains
L Infect. Immun. (1999) In press
E 2 (bases 1 to 525)
S Moe, G.R., Tan, S. and Granoff, D.M.
Direct Submission
Liect Submission
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Liectiute, 747 Fifty-Second Street, Oakland, CA 94609, USA
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/mol_type="genomic DNA"
/strain="M136"
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Matches:
Conservative:
Mismatches:
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Hominidae; Homo.

Is (bases 1 to 1487)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klauener, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Gasavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Toghellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Banchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Stalka, U., Samilus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
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VKGLVEIFGRETPVELSFDQIQKN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUNTEZU/
HOMO SABJENB hypothetical protein LOC348645, mRNA (CDNA clone IMAGE:5419610), partial cds.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (07-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                            /codon_start=1
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BC048207.1 GI:29387213
                 60. .962
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Query Match:
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AUTHORS
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REPERENCE
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VRSGELSAGVRVKF"
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1 (bases 1 to 1166)

Miyake,K., Onaka,H., Horinouchi,S. and Beppu,T.
Organization and nucleotide sequence of the secE-nusG region of Streptomyces griseus
Biochim. Biophys. Acta 1217 (1), 97-100 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NugG; transcription antitermination.
Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria, Actinobacteria, Actinobacteries,
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Organism="Streptomyces coelicolor A3(2)"
/mol_type="genomic DNA"
/strain="A3(2)"
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Mismatches:
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S.coelicolor gene for NusG, complete cds.
D17465
                                                                                                                                         /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 ProSerAlaSerAlaAlaAlaGlyIleAla 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CCTTCCGCCAGTGCGGCGCCGGGATAGCG 33
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Faculty of Agruculture
The University of Tokyo
Bunkyo-ku, Tokyo 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sub_strain="M130"
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/mol_type="genomic DNA"
/strain="NG3/88"
/db_xref="taxon:487"
1. .525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-989-890-238 (1-212) x AF175681 (1-525)
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03-3812-0544.
                                                                                   'gene="nspA"
                                                                                                                          gene="nspA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1166)
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Best Local Similarity:
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Pred. No.:
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TITLE
JOURNAL
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STMNUSG/c
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AUTHORS
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셤 8

PRI 09-SEP-2003

REMARK COMMENT

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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:genomicoshri.or.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NBDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA library

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5- c 3- end one pass sequencing:

RNI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawakami, B., Sugiyama, A., Takemoto, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai, Hio, Y., Salto, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. MEDO human cDNA sequencing project Unpublished

2 (bases 1 to 1635)
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Homo sapiens cDNA FLJ42972 fis, clone BRSTN2019129.
AK124962
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/clone lib="BRSTN2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK124962.1 GI:34530900
oligo capping; fis (full insert sequence).
Homo sapiens (human)
                                                                                   Matches:
Conservative:
Mismatches:
Indels:
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/note="unnamed protein product"
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Matches:
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                                                                                                                                                                                                                                    US-09-989-890-238 (1-212) x CQ841901 (1-1635)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="BRSTN2019129"
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Best Local Similarity:
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Pred. No.:
                                        Alignment Scores:
Pred. No.:
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AK124962/c
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JOURNAL
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Contact: MGC help desk
Email: cgapba-refmail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov
Contact: nisc mgc@nhgri.nih.gov
Contact: nisc mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.M., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Cuan,X., Gupta,J., Hadpighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 44 Row: h Column: 2.
Location/Qualifiers
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Full-length human cdna
Patent: EP 1440981-A 28-JUL-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5419610"
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Matches:
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Indels:
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Sequence 548 from Patent EP1440981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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Homo sapiens
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VERSION
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FEATURES

RESULT 20

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FEATURES

ORIGIN

TITLE

Query Match:

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

LOCUS DEFINITION

RESULT 22 BC079148

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PDPKDPGHHGPESITFISGSAEPANEPPTCCLLWRPWGWDWCRAAFCFRRCRDCLQRC
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THESDLDLPBMGSGSMSRELDVLIFTKKLTBELEVRYQIDELAKTTSDYVELKKYSKIS
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Homo sapiens forkhead box OlA (rhabdomyosarcoma) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae, Homo.

1 (bases 1 to 1968)
Kalnine,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y.,
Phelan,M. and Parmer,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 [(Dasse 1 to 1968)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Bisenstein, S.,
Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y.,
Phelan, M. and Farmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission

Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA

This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning of human full-length CDSs in BD Creator (TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="similar to hypothetical protein FLJ34633"
/product="almaH79148.1"
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                                                                                                                                                                      tissue type="Kidney, rat (Brown Norway)"
clone lib="NIH MGC_236"
lab_host="DH10B"
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                                                                                    mol_type="mRNA"
db_xref="taxon:10116"
clone="MGC:94165 IMAGE:7128510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
                                                            organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 GCTGCAGGATTGCCTCCAGCGCTGTGGAG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 AlaAlaGlyIleAlaSerSerAlaValGlu 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                    'note="Vector: pExpress1"
                                                                                                                                                                                                                                                                                                                     /gene="MGC94165"
/db_xref="GeneID:313018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-989-890-238 (1-212) x BC079148 (1-1718)
   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             gene="MGC94165"
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FLI_CDNA.
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DB:
                                    source
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SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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      FEATURES
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Riausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchencho, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loqquellano, N.A., Peters, G.J.,
Abramson, R.J., Mulahy, S.J., Bosak, S.A., McKernan, F.J., Mulyk, S.W.,
Worley, K.C., Hala, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
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Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                              BC079148 11near ROD 15-SEP-2004 Rattus norvegicus similar to hypothetical protein PLJ34633, mRNA (CDNA clone MGC:94165 IMAGE:7128510), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 184 Row: d Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                     Gaps:
                                                                                                                                           US-09-989-890-238 (1-212) x AK124962 (1-1635)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC079148.1 GI:50927712
MGC.
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Percent Similarity:
Best Local Similarity:
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REFERENCE AUTHORS TITLE JOURNAL

REMARK COMMENT

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Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD in-Fusion(TM) cloning system between the Sall and Hindlin sites of the pDNR-DDAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before Hindli site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trainiation="Maearqvveidpdfeplerrsctwplrefsgsnsatsspap
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LHSKFIRVQNEGTGKSSWWILNPEGGKSGKSPRRRAASMDNNSKFAKSRSRAAKKKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQSGQEGAĞDS PGSQFSKWPASPGSHSNDDFDNWSTFRPRTSSNASTI SGRLSPIMTE
DDDLGAEDUHSMYY PPEAARMASTLESEISEISTENENMENLLDNIALLISESPTSLITSTOF
SSPGTWMQQTPCYS FAP PNTSLIAS PSPRYQKTYTGGSSSMSPLPQMPIQTLQDNKSSYG
GMSQYNCAPGLLKELLTSDSPPHNDIMTPVDPGVAQPBNSRVLGQNVMMGPNSVNSTYG
SAGSHNKWMPESHTHPGHAQYTSANGRPLPHYVSTWPHTSGNNRLTQVKTPVQVPL
PHPMQMSALGGYSS VSSCNGYGRMGLI-HQEKLPSDLDGMFIERLDCDMESIIRNDLMD
GDTLDFNFDNVLPNQS PPHSVKTTTHSWVSG
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1 (bases 1 to 1968)

Hines, L., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Genudinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.

Cloning of human full-length CDS in Creator (TM) recombinational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1968)
Intesp., Rolfe, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F.,
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,
Williamson, J. and LaBaer, J.
                                                                                                                                                                                                                                                                                                                                                          'clone_lib="BD Creator(TM) CDS Library derived from MGC
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protein_id==RAP36123.1"
/db_xref="GI:30583749"
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'note="Vector: pDNR-Dual"
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-989-890-238 (1-212) x BT007455 (1-1968)
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Human ORF Project.
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Query Match:
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Pred. No.:
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9
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AUTHORS
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AY890173
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KEYWORDS
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Direct Submission
Submitted (04-JAM-2005) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141, USA
This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
This ORF clone has been cloned with normalized stop-codon. The CDS
has been directionally cloned using BD in-Rusion(TM) cloning system
between the SalI and HindIII sites of the pDNR-Dual vector.
Additional sequences in the clone: 'ACC' affer SalI site and
before 'ATG' to provide Kozak consensus sequence. Each clone is
Location/Qualifiers
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GNLS'YDLITKAIESSAEKTILLSOIYEWMYKSVPYFKOKGDSNSAGWKNSIRIRHULS
LHSKFIRVQNBGGTGSSWWLNPEGGKGSGSPRRAAABDNNSKFARARSRAAKKKAAS
LQSGQBGAGDSPGSOFSKWPASPGSHSNDDPDWSTFRPRTSSNASTISGELSPIWTE
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SSPGTWMQOTPCYSFAPPWTELNSPSPNYOKTYYGGSSMSPLDQMPTQTLQDNKSSYG
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PHPMQNSALGGYSSVSCNYGRMGLLHQEKLPSDLDGMFIERLDCDMESIIRNDLM
GDTLDPNFDNVLPNQSFPHSVKTTTHSWVSG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein id="AAX42115.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other sequences; artificial sequences.

1 (bases 1 to 1968)

1 Index D. Rolfs, Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Voundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and LaBaer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="Escherichia coli DH5alpha T1 resistant"
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Conservative:
Mismatches:
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|clone="FLH015808.01X"
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/transl table=11
product="forkhead box OIA"
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'gene="FOXO1A"
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                                                                                                                                                                                                               Direct Submission
Submitted (24-AUG-1993) Hiroyasu Onaka, The University of Tokyo,
Department of Biotechnology; Yayoi, Bunkyou-ku, Tokyo 113, Japan
(E-mail:aa57093@hongo.ecc.u-tokyo.ac.jp, Tel:03-3812-2111(ex.5147)
                                                                          MyAke,K., Onakk,H., Horinouchi,S. and Beppu,T.
Organization and nucleotide sequence of the secR-nusG region of
Streptomyces griseus
Biochim. Biophys. Acta 1217 (1), 97-100 (1994)
                      Bacteria; Actinobacteria, Actinobacteridae, Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Streptomyces griseus"
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|db_xref="GI:483835"
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Dept. of Aguricultural Chemistry
Faculty of Agruculture
The University of Tokyo
Bunkyo-ku, Tokyo 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:1911"
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      Streptomyces griseus
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                                                                                                                                                              8286423
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Phone:
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Shen, B., Rolfs, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, B., Williamson, J. and Labar, J.

Direct Submission

Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORR clone has been cloned with normalized stop-codon. The CDS has been directionally cloned with normalized stop-codon. The CDS has been directionally cloned with normalized stop-codon. The CDS has been directionally cloned with mormalized stop-codon. The CDS has been directionally cloned with sequence. This CDS clone is not between the Sall and Hindill sites of the pDNR-bual vector.

Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence. Each clone is clonally isoclated and full-length sequence-verified.
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Cloning of human full-length CDS in Creator (TM) recombinational
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| protein_id=*AAX42116_1"
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/gene="FOXO1A"
/note="rhabdomyosarcoma"
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KRLGYVYLHWULTIRESWGVRNTFGYTGFYGNAYDPYPLTLDEI VKNLAPERKNYRQ
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SOURCE ORGANISM

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Hominidae, Homo.

Straubserg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauseer, Homo.

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Earmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Wodin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, K.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunzarane, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Youchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M.I., Skalka, J., Schmutz, J., Myers, R.M., Butmalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (22-JNA-2002) National Institutes of Health, Mammalian Submitted (22-JNA-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:18314374.

Contact: MGC help deak

Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahney, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: o Column: 10.
Location/Qualifiers
                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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'gene="FOXO1A"
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     Sus scrofa forkhead/winged helix transcription factor FOXOla (foxola) mRNA, complete cds.
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Homo sapiens forkhead box OlA (rhabdomyosarcoma), mRNA (cDNA clone MGC:1750 IMAGE:2959021), complete cds.
                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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TALQVPLPHPMQMNALGGYSPASTCNGYGRMGLLHQEKLPSDLDGMF1ERLDCDMES1
IRNDLMDGDTLDFNFDNVLPNQSFPHSVKTTTHSWVSG"
                                                                                                                                                                                                                                                                                                                                                        Zhu,Q., Cunningham,M.A. and Hammond,J.M.

FKHR Expression in Porcine Granulosa Cells
Unpublished
2 (bases 1 to 2162)
Zhu,Q., Cunningham,M.A. and Hammond,J.M.

Direct Submission
Direct Submission
Submitted (02-APR-2002) Dept. of Medicine/Div. of Endocrinology,
Pennsylvania State Univ. College of Medicine, 500 University Dr.,
Hershey, PA 17033, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="forkhead/winged helix transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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BC021981.2 GI:33869892
MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="foxola"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33. .2021
/gene="foxola"
                                                                                                                                                     AY094061.1 GI:20384962
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                                                                                                                                                                                                        Sus scrofa (pig)
Sus scrofa
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Contact: MGC help desk
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18 I (bases 1 to 2482)

Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Onnes, S. J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and intital analysis of more than 15,000 full-length
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TGGLCGDFQGPEAGCLHPAPPOPPPFGCLSGIPPVPPAAAGPRKSSSSRRNAW
GNLSYADLITKAIESSAEKRLTLSQIYEWWYKSVPYFWDKGDSNSSAGWKNSIRHNLS
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PHPMQMSALGGYSSVSSCNGTGRMGLHQBKLPSDLDGWFIERLDCDMESIIRNDLMD
GDTLDFNPDNVLPNQSFPHSVKTTTHSWVSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2482 bp mRNA linear PRI 21-JUL-2005 Homo sapiens forkhead box OlA (rhabdomyosarcoma), mRNA (cDNA clone IMAGE:30345006), partial cds.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Submitted (10-MAY-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nlh.gov
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BC070065.1 GI:47123315
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CONSRTM
TITLE
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at: http://image.llnl.gov Series: IRAK Plate: 168 Row: n Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9257221. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / CTAINSTALL OID = "HSTGSSAAGAPLGRASGPRRPSVLPSAALSAGARRILCPGPAAL
AGRPVRAADAPASFOCGURSTBURKEWARASTPPRILEPSRRLLAAPASFOCGSBRPAPBP
ROPPVLKSPPLGSPAAGGAGVTWAABAPQVVBIDPDFBLPRRRCTWPLPRBEFSOS
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KNSIRNNLAABAATGLSHBKFTITALISGIYEWWYKSVPYFKDKGDSNSSAGM
KNSIRNNLAABAATGLSHBKFTITALISGIYEWWYKSVPYFKDKGDSNSSAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRAAKKKASLOSGQEGAĞDSPGSQFSKWPASPGSHSNDDFDNWSTFRPRTSSNASTIS
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LQDNKSSYGGANSQYNCAPGLLKELLISDSPPHNDIMTPVDPGVAQPNSRVLGQNVMG
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VKTPVQVPLPHPMQMSALGGYSSVSSCNGYGRMGLLHQEKLPSDLDGMF1ERLDCDMB
                                                                                                                                                                                 94305
                                                                                        Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943(
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
Bmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIIRNDLMDGDTLDFNFDNVLPNQSFPHSVKTTTHSWVSG"
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Mismatches:
Indels:
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/clone lib="NIH MGC 147"
/lab host="DH10B"
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db_xref="GeneID:2308"

db_xref="MIM:136533"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="FOXO1A protein"
/protein id="AAH70065.2"
/db xref="Gi=171052130"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'clone="IMAGE:30345006"
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Submitted (20-JUL-1994) Chunya Puttikhunt, Osaka University, Department of Biotechnology; 2-1 Yamadaoka, Suita, Osaka 565, Japan (Tel:06-877-5111(ex.3441), Fax:06-879-7448) Submitted (20-Jul-1994) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                             TVPSPQRSAPRASLCPPHKGQHPEHHCALPPKGQHPEHHCALPTKVSTPSITVPSPQR
SPMGILSSARGSNTDVAGLSVGEWPKOQLWGBGQDGAQQRPHLPSGGSGGAGVARQRL
PKSBACILCSRHGAGEWYYGRSVSHSHCPIQGLLDLQRPDLGTDWGRTRPLCTPQDL
CGGRPLPSTWGVTWHLIHCLSVSLSLCLSLSHCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCT 02-SEP-1997
                                                                                                                                                                                                                                                                                                                                             translation="MPILQALCLLPKVSTPSITVPSPQRSAALSITVPSPQRSAAPSI/
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1 (bases 1 to 2981)

Puttikhunt, C., Nihiza, T. and Yamada, Y.
Cloning, nucleotide sequence, and transcriptional analysis of the mused gene of Streptomyces coelicolor A3(2), which encodes a putative transcriptional antiterminator

Mol. Gen. Genet. 247 (1), 118-122 (1995)
Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STMSAM 2981 bp DNA linear BCT 02-SI
Streptomyces coelicolor DNA for aspartate
aminotransferase,ribosomal protein, partial and complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                          tissue type="uterus"
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                                              Location/Qualifiers
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Department of Biotechnology
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Direct Submission
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                                                                                                                                                                                                                                   Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.
Full-length human cdna
Patent: EP 1440991-A 2100 28-JUL-2004;
Research Association for Biotechnology (JP)
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  PAT 02-AUG-2004
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Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Cmura, Y., Abe, K.,
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NEDO human cDNA sequencing project
Unpublished
                                                                                                                                                    Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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    linear
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Matches:
Conservative:
Mismatches:
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    2816 bp
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Isogai, T. and Yamamoto, J.
Direct Submission
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                                            CQ843453
CQ843453.1 GI:50895240
                                                                                                          Homo sapiens (human)
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Best Local Similarity:
Query Match:
    20843453
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AK126430/c
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Human fork head domain protein (FKHR) mRNA, complete cds.
U02310 GI:435422
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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codon_start=1
evidence=not_experimental
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complement(<1. .368)
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2244. .2678
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Matches:
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Mismatches:
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Matches:
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Mismatches:
Indels:
Patent: WO 2005016962-A 687 24-FEB-2005;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 687 from Patent WO2005019258.
CS040133
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synthetic construct
other sequences; artificial sequences.
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Sequence 134 from Patent W00246467.
AXS87664
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Location/Qualifiers
              Inc. (US)
Location/Qualifiers
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Best Local Similarity:
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CSO40133
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                                FEATURES
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Submitted (01-0CT-1993) Naomi Galili, Wistar Institute, 3606 Spruce
Street, Philadelphia, PA 19104 USA
Location/Qualifiers
1. 3421
/organism="Homo sapiens"
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1. 3421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALLSTATELLITKALIESABKRALTILĞQIYERMYKSVPYFOKGOSNUSSAGWKNISTERNIZ
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                                                                                            Galili, M.
Pusion of a fork head domain to PAX-3 in the solid tumor alveolar Thabdomyosarcoms
Nature Genetices 5(3), 230-235 (1993)
2 (bases 1 to 3421)
2 (bases 1 to 3421)
Galili, N., Davis, R.J., Fredericks, W.J., Mukhopadhyay, S.,
Rauscher, F.J. III, Emanuel, B.S., Rovera, G. and Barr, F.G.
                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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protein id="AAA03629.1"
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Sequence 687 from Patent WO2005016962.
CS031181.1 GI:60731351
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                                                                   Hominidae; Homo.
1 (bases 1 to 3421)
sapiens (human)
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                   Homo sapiens
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PAT 22-MAR-2005

Wu, T.D

PAT 10-JAN-2003

linear

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LQSGQEGAGDSPGSQPSKWPASPGSHSNDDPDNWSTPRPRTSSNASTISGRLSPIMTE
DDDLGSEDVHSHVYPPRAAKAGASTLSBSLSRSBENBENBUNLDLDNLALLSBSPTSLTVSTQ
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GDTLDFNFDNVLPNQSPPHSVKTTTHSWVSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S., Dugaa,M., Eils,R., Brors,B. and Mergenthaler,S.
Novel genetic markers for leukemias Patent: W. 0.3039443-A. 2147 15-WAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE); Haferlach, Torsten, PD Dr. (DF); Schoch, Claudia (DE);
Location/Qualifiers
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Mismatches:
Indels:
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X72787.1 GI:575399
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Matches:
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    /db_xref="taxon:9606"

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AX779990
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1. .5723
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                                Gene expression profiling of primary breast carcinomas using arrays of candidate genes
Patent: WO 0246467-A 134 13-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF012885
Homo sapiens forkhead protein (FKHR) mRNA, complete cds.
AF032885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

1 (Dasea 1 to 5723)

Anderson, M. J., Viars, C. S., Czekay, S., Cavenee, W. K. and Arden, K. C. Cloning and characterization of three human forkhead genes that comprise an FKHR-like gene subfamily Genomics 47 (2), 187-199 (1998)
9479491
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Anderson, M.J., Viars, C.S., Czekay, S., Cavenee, W.K. and Arden, K.C. Direct Submission
Submitted (03-NOV-1997) Medicine, Ludwig Institute for Cancer Research, San Diego Branch, 9500 Gilman Drive, La Jolla, CA
Bertucci, F., Houlgatte, R., Birnbaum, D., Nguyen, C., Viens, P.
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Matches:
Conservative:
Mismatches:
Indels:
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10.00
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VERSION
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Cloning and transcriptional analysis of the rplKA-or f31-rplJb gene
cluster of Streptomyces griseus
MMO1. Gen. Genet. 257 (2), 219-229 (1998)
9491081
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The nusG gene of Streptomyces griseus: cloning of the gene and analysis of the A-factor binding properties of the gene product FEMS Microbiol. Lett. 119 (1-2), 33-39 (1994)
                                                                                              Streptomyces griseus
Streptomyces griseus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                              L12; rplA gene; rplJ gene; rplK gene; rplL gene; secE gene; tRNA-Trp gene.
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Homo sapiens chromosome 8 clone RP11-68J16 map 8, LOW-PASS SEQUENCE
SAMPLING.
AC137577
AC137577.1 GI:25229244
HTG; HTGS PHASE0.
Homo sapiens (human)
FALGVDPRKADQMVRGTVNLPHGTGKTARVLVPATGDRAAABAAGADI VGADELI DE
VAGRALDFDRAVVATPDLMGKVGRLGRVLGPRGLMPNPRTGTVTPDVVKAVNDI KGGKI
BFRVDKASNLHFI I GVEVS PDETKLVENYAAALBE I LRLKPSAAKGRY I KKATLATTMG
PGI PLDANRTRNLLVBEDPASV"
                                                                                                                                                                                                                                                                     /translation="MRTSTARRTGTALAVAAALTSIAACSGSDGAKGSDGACGGKAGA
VSKASPVAALKQVQOKTGGAQSAKVEGTTEMGSVMSMKQSGAIGWADGLSGALTITYT
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GDVMKDQIQNSTPEGGVKALLASGDVKKVGQEDVRGVPATHYSGTVDVAGLTAKNSNL
DABQLAAFKEQLAALGAVTTQTVDIWVDKNDLLVKKTERGEMKTGSFNSTIFYSDYGTE
VPTEKPAASDTVDFKEMLKQGGATPGATS"
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                                                                                                                                                                                                                                            db_xref="InterPro:IPR000437"
db_xref="UniProt/Swiss-Prot:P36261"
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Matches:
Conservative:
Mismatches:
Indels:
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protein id="CAA51300.1"
                                                                                                                                                                          note="putative lipoprotein"
codon start=1
fransl_table=11
protein_id="CA51299.1"
db_xref="GI:575402"
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                                                                                                            note="putative lipoprotein"
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5039. .5043
/gene="rplJ"
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                                                      3786. .4779
/gene="orf31"
3786. .4776
/gene="orf31"
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trans table=
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/gene="rplJ"
5055. .5612
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|qene="rplJ"
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Best Local Similarity:
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KEYWORDS
SOURCE
ORGANISM
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AC137577/c
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2 (Dases 1 to 08170)

Barran, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barren, B., Nusbaun, C., Lander, B., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Chospel, Y., Collymore, A., Cooke, P., DaArellano, K., Dawar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J. Gardhan, C., Grand-Pierre, N., Hafez, N., Hafez, N., Hales, M., Hales, M., Hafez, N., Haleyos, B., Horton, L., Hulm, W., Iliev, I., Lowine, R., Jones, C., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Malor, T., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Menders, T., Levine, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Loure, T., O'Donnell, P., O'Neil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Connor, T., O'Donnell, P., O'Neil, D., O'Connor, T., O'Connor, T., O'Connor, T., O'Donnell, P., O'Neil, D., O'Connor, T., O'Connor, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Viel, R., Wilson, B., Wu, X., And C., Connor, T., O'Connor, J., Connor, J., Mallon, B., Wu, X., Milson, B., Wu, X., Milson, B., Wu, X., Milson, B., Milt, A.F., & Green, P. (1996, 1997)

All repeats were identified using RepeatMasker:
Salt, A.F., & Green, P. (1996, 1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence submissions@genome.wi.mit.edu ------ Project Information Center project name: L28701 Center clone name: 68_J_16
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gap of 100 bp
contig of 695 bp in length
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Homo sapiens chromosome 8, clone RP11-68J16
Unpublished
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                                                                                                                                              (bases 1 to 68170)
                                                                                                                                                                                                                                                                                                                                          (bases 1 to 68170)
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3937:
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: gap contig of 696 by ...
: gap of 100 bp

8: contig of 692 bp in length

8: gap of 100 bp

8: gap of 100 bp
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9352:
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10131:
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14084:
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LOCUS BA000002 Accession BA000002
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Matches:
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Mismatches:
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BA010002_16
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BA010002_16
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1. 5913
1. force="assembly_fragment:00193
fragment chain:1"
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hote="assembly_fragment:00080
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hote="assembly_fragment:00049
fragment chain:1"
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fragment chain:1"
50113. .52494
/notes"assembly_fragment:00041
fragment chain:1"
52595. .55884
/notes"assembly_fragment:00069
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/db_xref="taxon:7955"
/clone="DKEY-5848"
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/organism="Danio rerio"
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                               11-4 400001 410877
CR555291 410877 bp DNA linear HTG 11-OCT-2004
Danio rerio clone DKEY-58J8, *** SEQUENCING IN PROGRESS ***, 37
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 17, 2004 this sequence version replaced gi:50724921.
                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygli; Neopterygli; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 410877)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 394129 bases at least Q40
Consensus quality: 399430 bases at least Q40
Consensus quality: 402692 bases at least Q20
Insert size: 407277; sum-of-contigs quality coverage: 200961; 2.9% error; agarose-fp
Quality coverage: 4.75x in Q20 bases; sum-of-contigs Quality
coverage: 9.83x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Contact: zfish-help@sanger.ac.uk
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CRS55291.4 GI:52313314
HTG; HTGS PHASE1.
Danio rerio (zebrafish)
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Library Commission Wellcome Trust Sanger Institute, Hinxton, Cambritdgeshire, CB10 18A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: cloneerquest@sanger.ac.uk clone requests: cloneerquest@sanger.ac.uk

On Dec 13, 1999 this sequence version replaced gi:2996576.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw.; SWISSROT; Tr.; TREMBL; Wp:, WORMPEP; Information on the WORWPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Purther information can be found at http://www.aanger.ac.uk/HGP/Chr22

RRP1-29C18 is from the library RPCI-1 constructed by the group of Pieter de Jong. Por further details see http://www.chori.org/bacpac/home.htm
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119033. .119166)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
           3ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
4ammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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standard_name="OTTHUMP0000028703"
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Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
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Human DNA sequence from clone RP1-29C18 on chromosome 22, complete
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                                                                                                                                         gene
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Submitted (13-MNY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk Cnne requests: clonerequest@sanger.ac.uk on Sep 20, 2001 this sequence version replaced gi:15020887.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 http://www.sanger.ac.uk/HGP/Christ Chromosome 13 http://www.sanger.ac.uk/HGP/Christ RPI1-181D10 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                              AL355132 I51261 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RP1-1181D10 on chromosome 13 Contains a ring finger protein 12 (RNF12) pseudogene, the 5' end of the FOXO1A gene for forkhead box O1A (rhabdomyosarcoma), the 3' end of the MRPS31 gene for mitochondrial ribosomal protein S31 and a CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chamistry or covered by high quality data of i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL355132.19 GI:15717908
HTG; CpG island; FOXO1A; MRPS31; RNF12.
HOmo sapiens (human)
Homo sapiens
                                                                                                                                                             Mismatches:
Indels:
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VECTOR: pBACe3.6
                                                                                                          US-09-989-890-238 (1-212) x HS29C18 (1-143701)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae, Homo.
1 (bases 1 to 151261)
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  100.0%
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Best Local Similarity:
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                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Backer, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Berreitas, P., Fitzhugh, W., Forrest, C., Funke, R., Herena, L., Horton, L., Howland, J.C., Jacotto, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Wychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Ve, W., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.
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                                                                                                                                                            ACO05901 156763 bp DNA linear PRI 20-JAN-1999
Homo sapiens chromosome 17, clone hRPK.15_K_2, complete sequence.
AC005901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-OCT-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 156763)
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1 (basea 1 to 15673)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.15_K_2 Unpublished
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    156763
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                               HIG.
                                                                                                                                                                                                         DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                         RESULT 47
AC005901/c
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TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                         gene="MRPS31"
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1044. .22134
'rpt_family="L1M4"

rpt_family="L1M4"

ronce="Single-stranded terminator coverage."

1182. .21882. .21886

note="Three subclones have four T's here; one subclone as five T's here."
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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25593. .25861
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complement (26380. .26676)
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complement (26380. .26676)
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complement (27262. .27464)
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/rpt family="Trigger1"
/rpt family="Trigger1"
complement(31282. .31557)
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Complement (27739. .27786)

Art family="Alusx"

Art family="71961"

Complement (27780. .28199)
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. .28274
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/rpt family="LiPAl6"
28275. 28316
/rpt family="(CA)n"
28317. 30059
/rpt family="LiPAl6"
30080. 30372
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19637. .13391
19637. .19391
19663. .19936
/*TPL family="WRR20"
19866. .19936
/*TPL family="L2"
20206. .20319
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20402. .20568
/*TPL family="HAL1"
20914. .21001
/*TPL family="HAL1"
17921. .18041
/rpt_family="GA-rich"
18870. .19391
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    /clone="hRPK.15 K 2"
/clone_lib="RPCI-11 human BAC library"
...59
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/rpt family="Aluxb8"
complement (11613. .11702)
/rpt family="MIR"
complement (11873. .12179)
/rpt family="Aluxx"
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complement(15736..16045)
/rpt_family="AluSx"
complement(16701..16813)
/rpt_family="MIR"
16929..17231
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3394. .13435
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6485. 6765
6765. 6765
6766. 6792
/rpt family="AluSx"
6766. 1792
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2792. .2846
/ rpt family="AT rich"
2003]ement (2847. .3643)
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complement (3864. .3770)
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3868. .3894
/ rpt family="L2"
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4381. .4881
/ rpt family="L1PA8"
4381. .4841
/ rpt family="L1PA8"
4381. .5160
/ rpt family="L1PA8"
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13780. 13800
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14820. 15103
                                                       rpt_family="AluJ/FRAM"
0. .79
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17615. 17920
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165. .1448
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/rpt_family="(CA)n"
15156. .15186
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rpt_family="LIMC2"
976. .6441
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases:

Em:, EMBL; Sw:, SWISSERCY; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of monoucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR846094 175626 bp DNA linear VRT 26-MAY-2005
Zebrafish DNA sequence from clone CH211-264F16 in linkage group 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-264F16 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Submitted (16-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Zambridgeshire, CB10 15A, UK. E-mail enquiries:
zfish-help@asanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 22, 2005 this sequence version replaced gi:66351741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Schinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyptiniformes; Cyptinidae; Danio.

    (bases 1 to 17528)

                                                                                                                                                      Conservative:
  /note="assembly_fragment:00052"
                                                                                                                                                                           Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                           52087 CTCTCCAGACCACTAAGTCCGCCGCCTGCG 52058
                                                                                                    Length:
Matches:
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Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR846094.7 GI:66392950
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Best Local Similarity:
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                                                                         Alignment Scores:
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SOURCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR846094
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174869 bp DNA linear HTG 23-JUN-2005
Danio rerio chromosome 24 clone DKEYP-122B1, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (16-JUN-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 15A, UK. E-mail enquiries:
zfish-help@eanger.ac.uk Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 96348: contig of 96348 bp in length
3349 96448: gap of 100 bp
449 153731: contig of 57283 bp in length
153721: santig of 57283 bp in length
1832 157656: contig of 3795 bp in length
1627 157726: gap of 100 bp
1777 174869: contig of 17143 bp in length.
10cation/Qualifiers
                                                                                                                                                                                  CR936217.2 GI:68162272
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
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153822. 155626
/note="assembly fragment:00001.0"
157727. 174869
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fragment_chain:1"
96449. .153731
113671 GCCCTGCCTCCAGCCTGGCTCTTCC 113642
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1. .96348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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AC124555 210174 bp DNA linear ROD 01-JAN-2004
Mus musculus BAC clone RP23-245Kl7 from chromosome 14, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                  **NOTE: This is a 'working draft' sequence. It currently
** consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 117197 117196: contig of 117196 bp in length
* 117297 199160: contig of 81864 bp in length.
* Location/Qualifiers
* ce /organism="Canis familiaris"
/ mol type="genomic DNA"
/ db xref="taxxon:9615"
                   clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a phrap-derived quality score.
                                                                                                                                                                                                Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 19826 bases at least Q40
Consensus quality: 198947 bases at least Q20
Consensus quality: 199018 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 199060; sum-of-contigs
Quality coverage: 13.82x in Q20 bases; agarose-fp
Quality coverage: 12.84x in Q20 bases; sum-of-contigs
data from individual subclones, overlaps with neighboring
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/clone_lib="RP81"
1. .1171966
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117197. .117296
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Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Cariadag, K., Coleman, B., Engled, G. Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J. R., Karlins, E.,
Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,
Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A.,
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,
Wetherby, K.D., Wigglis, L., Young, A. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC137538 199160 bp DNA linear HTG 18-DEC-2002
Canis familiaris clone RP81-349K11, WORKING DRAFT SEQUENCE, 2
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Submitted (12-NOV-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 199160)
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Web site: http://www.nisc.nih.gov
Contact: nisc zoo@nhgri.nih.gov
Contact: project Information
Center project name: dgr
Center clone name: 349K11
                                                                                                                                                                                                                                                                                                                                                                                                                                     31 LeuSerArgProLeuSerProProAla 40
                                                                                                                                                                                                                                                                                                                                                                                        US-09-989-890-238 (1-212) x CR846094 (1-175626)
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                                                                                                                                                                                                                                                                                                                                               Gaps:
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HTG; HTGS PHASE2; HTGS_DRAFT.
Canis familiaris (dog)
Canis familiaris
Location/Qualifiers
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432I. .14508
note="Sequence derived from PCR product of project DNA."
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       1. .210174
/organism="Mus musculus"
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                                                                                                                                      clone="RP23-245K17"
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21743. 21980
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22601. 22673
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23916. 24235
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12120 . 12350
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12351 . 12739
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164. .3207
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3064. .13127
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735<u>9</u>. .17656
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8207. .18276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 8, 2003 this sequence version replaced gi:31880269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 210174)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (08-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 210174)
Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-JUN-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 210174)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidae, Muridae, Murinae, Mus.
1 (bases 1 to 210174)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                       The sequence of Mus musculus BAC clone RP23-245K17
Unpublished (2001)
2 (bases 1 to 210174)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: M_BA0245K17
                                                                                                                                                                                                                                                                                            3 (bases 1 to 210174)
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                    Kruchowski, S. and Haakenson, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- Genome Center
                                                                                                                                                                                                                                                Sequencing of Mus musculus Unpublished (2001)
musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://genome.wustl.edu
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                                                                                                                                                                                                                             Wilson, R
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TITLE

COMMENT

JOURNAL REFERENCE This sequence is the entire insert of the clone. Location/Qualifiers

NEIGHBORING SEQUENCE INFORMATION:

24257. .24382 /rpt_family="L1" 24401. .24541 /rpt_family="Alu" 24577. .24717

rpt_family="L1"

repeat_region repeat_region repeat_region repeat_region

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(bases 1 to 216621)
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Matches:
Conservative:
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/rpt_family="B4"
30599. 30798
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0799. .30869
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KEYWORDS
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Muzny, D., Adams, C., Agbai II.O., Allen, C., Alsbrooks, S., Archer, P., Arredondo, H., Bandaranaike, D., Bangura, L., Beltran, B., Beltran, R., Arredondo, H., Bandaranaike, D., Bangura, L., Beltran, B., Beltran, R., Cadorce, I., Canda, A., Cardenas, V., Carter, K., Cavazos, I., Chard, D., Chen, B., Chen, B., Chen, C., Chen, B., Chen, C., Chen, Direct Submission
Submitted (30-MAY-2005) Human Genome Sequencing Center, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 30, 2005 this sequence version replaced gi:63253308.
Sequencing is completed to a minimum standard of double strand
coverage with a minimum of 2 clones and 2 reads with no ambiguities
or 2 chemistries with a minimum of 2 clones and 3 reads with no
ambiguities. If the sequence quality does not meet this standard,
it will be indicated in the annotation. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Worley, K.C.
Direct Submission
Submitted (23-MAR-2005) Human Genome Sequencing Center, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 216621) Direct Submission Submitted (12-MXY-2005) Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 4 (bases 1 to 216621) Sciurognathi, Muridae; Murinae; Mus. 1 (bases 1 to 216621)

The repeat regions shown were identified using RepeatMasker by

Sequence similarities were identified using Powerblast by Jinghui

Mus musculus (house mouse) Mus musculus

ORGANISM

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LK/92443 217987 bp DNA linear VRT 10-AUG-2005 Zebrafish DNA sequence from clone DKBY-52K1 in linkage group 13, complete sequence.
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Danio rerio (zebrafish)
Danio rerio
Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Ostariophysi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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complement(11013. 11211)
/rpt_family="ORR1A1"
11535. 11584
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complement(12498. .13439)
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complement(14491. 14610)
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omplement (11933. 12025)
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1628. .11752
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CR792443
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                        'clone="RP23-197F5"
1. .15082
hnote="overlaps bases 146386. .161467 of clone AC155323"
function="clone overlap"
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complement(5597. .6015)
/rpt_family="RWER12"
6016. .615?
                                                                                                                                                                                                                                                                                               735. 1122

/rpt family="MTA Mm"

complement (1436. 1967)

/rpt family="RLTR42-int"

complement (2027. .2136)

/rpt family="PBID9"

2249. .2295
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6153. 6192
/rpt_family="Rl_Mus2"
6193. 6203
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complement (6204. 6506)
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complement (4694. 4950)
Crypt family="RLTR42-int"
complement (4969. 5152)
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/rpt_family="(CAAAAA)n"
complement(3705. .4352)
/rpt_family="Li_Musl"
4518. .4544
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/db_xref="taxon:10090"
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omplement (2719. .2786)
rpt family="B1 Mue1"
omplement (2787. .2862)
                                                                                                                                                                                                                                                                                                                                                                                                           rpt family="(TG)n"
omplement (2296. .2354)
rpt family="81_Mm"
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779_.6842_.1014
770_.6843_.1014
6843_.7014
77017. .7065
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Direct Submission
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                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNPEP; Information on the WORNWEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep clone-derived Zebrafish puc subclones occasionally display inconsistency over the length of monounclectide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Any regions longer than 1kb tagged as misc-feature 'unsure' are part of a tandem repeat of more than 10kb in length where it has not been possible to annofor the base differences between repeat copies. The region has been built up based on the repeat element to match the total size of repeat indicated by restriction digest, but repeat copies may not be in the correct order and the usual bKEY-SZKI is from a Zebrafish BAC library

VECTOR: PIndisplace.
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Mus musculus 10 BAC 280B6 (Roswell Park Cancer Institute Human BAC
                                                                                     Submitted (10-AUG-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests:
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                                                                                                                                                                                                                                                                         Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Cypriniformes; Cyprinidae; Danio. (bases 1 to 217987)
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/db_xref="taxon:7955"
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/clone lib="DanioKey"
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complement(14808 .14899)
/rpt_family="LM4"
complement(14979 .14989)
/rpt_family="LM4"
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5124. 5170
/rpt_family="0 (GTTTG)n"
complement (5171. 5216)
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/rpt_family="B1 MM"
complement(16451..16770)
/rpt_family="Lx3"
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/rpt_family="RMER1B"
complement(13888. .14086)
/rpt_family="ORRIA1"
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complement(15369..16281)
/rpt_family="Lx3"
/rpt_family="Lx3"
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12317. 12380
12584. 12584. 12584
/rpt_family="L2"
12681. 12731
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/rpt_family="(TTTA)n"
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omplement(14667...1
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| Ppc family="Bl_MM"

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| Ppc family="Cahahan" |

| Ppc family="Cahanin" |

| Complement (20666 . 20823) |

| Ppc family="RD" |

| Ppc family="RD" |

| Ppc family="Cahanin" |

| Ppc family="Caha
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Rattus norvegicus clone CH230-11020, WORKING DRAFT SEQUENCE, 3
unordered pieces.

AC095979

AC095979.7 GI:24818145

HTG5 HTG5 PHASE1; HTGS DRAFT, HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/ppt family="Bl_MW"
17488. .17531
/rpt family="CCA)n"
18519. .18569
/rpt family="RMBR17C"
/rpt family="CT-rich"
20083. .20228
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complement(17055..17307)
/rpt_family="84A"
17309..17365
/rpt_family="C-rich"
complement(17366..17485)
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complement (16820. .16954)
/rpt_family="B1_MM"
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                                                  Still Grades I to 23549)

Still Cognation, Mileotoes a Miritaes Matches; Ratches

Still Cognation, Mileotoes and Miritaes; Ratches

Allen, C., Allen, H., Alsbrooks, S., Admin, A., Angulano, D.,

Allen, C., Allen, H., Alsbrooks, S., Admin, A., Angulano, D.,

Anyalebechit, V., Aoyagi, A., Ayodeli, M., Barnstead, M., Benhamed, F.,

Baldwin, D., Bandsranike, D., Barber, M., Barnstead, M., Benhamed, F.,

Baldwin, D., Bandsranike, D., Barber, M., Barnstead, M., Benhamed, F.,

Bayant, M., Bular, C., Blarken, M., Barrstead, M., Chen, Z., Chu, J.,

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Bayan, A., Dugan, Rocha, S., Duny, M., Porber, J., Bayer, R.,

Eraser, C., Chon, G., Chen, R., Garler, M., Cherer, M., Guner, P.,

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Rockeon, L., Shvartesboyn, A., Rose, M., Reber, R., Sager, R.,

Reilly, B., Reilly, S., Tho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (109-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houeton, TX 77030, USA
Daylor Plaza, Houeton, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:22772470.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
Submitted (17-582-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                    Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 235419)
Rat Genome Sequencing Consortium.
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AUTHORS
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JOURNAL
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AUTHORS
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JOURNAL
                                                                 REFERENCE
                                                                                                        AUTHORS
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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole senome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap, version 0.990329
Consensus quality: 225536 bases at least Q40
Consensus quality: 227458 bases at least Q30
Consensus quality: 228649 bases at least Q20
Estimated insert size: 235033; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 221492: contig of 221492 bp in length 3 221522: gap of unknown length 3 228651: contig of 7059 bp in length 2 228751: gap of unknown length 2 235419: contig of 6668 bp in length. Location/Qualifiers
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                   Center: Baylor College of Medicine

    .235419
    /organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                             Center project name: GEBU
Center clone name: CH230-11020
----- Summary Statistics
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                                                                                                                                                                                                                                                                                      Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end_sequence:BH344795"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end_sequence:BH344813"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2958. .3664
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4.78
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228652
228752
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table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3666. .4538
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                                                     BCT 16-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCO4412"
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/note="SC6F11.10, possible regulatory protein, len: 163
asi similar to TR.02EDT (EMBL:A014446) Streptomyces
coelicolor putative regulatory protein SC1A9.20, 135 asi
fasta scores: opt: 227 z-score: 286.6 E(): 1.8e-08; 43.0$
/codon statt=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCO4413"
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regularory protein, len: 344 aa; highly similar to
TR:09S166 (EMBL:AB023785) Streptomyces griseus AdpA, 405
aa; fasta scores: opt: 881 z-score: 1024.1 E(): 0; 46.9$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces Sequencing team, Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: sdb@eanger.ac.uk
On or before Oct 26, 2002 this sequence version replaced
gi:11595527, qi:7242710, gi:7248323, gi:20520808, gi:7981386,
Location/Qualifiers
  248550 bp DNA linear BCT 16-APR-
Streptomyces coelicolor A3(2) complete genome; segment 17/29.
AL939120 AL078618 AL160312 AL160431 AL353815 AL356334 AL392146
AL392148 AL392175 AL392176 AL392178 AL645882
                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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/mol_type="genomic DNA"
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406. .897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 417 (6885), 141-147 (2002)
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406. .897
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Streptomyces coelicolor A3(2)
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RESULT 56
SC0939120/c
                                                                     DEFINITION
                                                                                                                                                                                                                                 ORGANISM
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(EMBILALIATOR) Streptomores coelistoor puteits decreased transcriptional regulator SCRP4.20c, 337 aas feate accreased copt: 1207 x=000ce: 1238 x=000ce: 1238 x=000ce: 1238 x=000ce: 1238 x=00ce: 1238 x=
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DEFINITION
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                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                          AUTHORS
GAGODDHGRGGGAFGVLCLPIVILDHOVHSSAQINDATLARLIPERSGPENARHVY
ASVLVGAGWAVLGHLVWGWPPRDTVPWFAGAGILPVILFAPLRAFRLARGSSPENARHVY
ASVLVGGGGGAAVAALADEYEPPALSDGQLAGSWRGDHGAYLRLAPGRRAWGGWSVWLRSAG
APPGTYRDYTRCSGTGTWSRNLSGDRBGVVVRLDGDGGEETSWTIGGSERSPELFALF
GDPDAGDLLFLTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SC6F11.15, probable acetyltransferase, len: 205 aa; similar to SW:RIML_ECOLI (EMBL:X15860) Escherichia coli similar to SPORTE ESSTING ACCETYLIANSFERASE (EC 2.3.1.-) RimL, 179 aa; fasta scores: Opt: 199 z-score: 261.1 E(): 4.8e-07; 30.6% identity in 157 aa overlap. Contains Pfammatch to entry PF00583 Accetyltransf, Accetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRSTAGWAAQYTGVLCRRLPVALVDRLARPLARISVPDLSAQGLPRPGTGLYSRVAEG
AIPVQDVGLIDAVRSGRVEVVVAAMDGPEDGKVLLADGTRIAPDAVIAATGYRRGLEGL
VGHLGVLDGTGRPVVQGGRTPAAAPGLYFTGPTNPISGMLRELAIDAERIAGAVAKRG
                                                                                                                                                                                                                                                     /note="SC6F11.14c, probable monooxygenase, len: 401 aa, similar to TR:QSSDE6 (EMBL:AP000837) Oryza sativa similar to human dimethylanilyne monooxygenase, 437 aa, fasta scores: opt: 692 z-score: 722.8 E(): 9.3e-33; 38.2% identity in 403 aa overlap. Contains Pfam match to entry PF00743 FMO-like, Flavin-binding monooxygenase-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tränglation="MADSTASAEPQRPTHPAGRPVYVIGAGPGGLAVAHALRARGLRA
VVLERADHVGSSWRRHYDRLRLHTTRRLSALPGLPIPRRFGRWVARDDVVRYLEKYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIQLEIVTGVEVFRVERAPDGTGWLLHAAGGRELTGAAVVVATGYNHTPRVPDWPGRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Pfam match to entry PF00743 FMO-like,
Flavin-binding monooxygenase-like, score -255.00, E-value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="CQA:Q9F372"
/db_xref="InterPro:IPR000103"
/db_xref="InterPro:IPR000205"
/db_xref="InterPro:IPR000759"
/db_xref="InterPro:IPR001327"
/db_xref="InterPro:IPR001327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="putative monooxygenase"
protein_id="CAC08425.1"
db_xref="G1:10178387"
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Matches:
Conservative:
Mismatches:
Indels:
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complement (4721. .5926)
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                                                                                                                               complement (4721. .5926)
/gene="SCO4416"
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trans1 table=11
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/gene="SCO4417"
                                                                                                                                                                                                                                   gene="SCO4416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5026. .6643
/gene="SCO4417"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=
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DB:
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243017 GGCGCCGGCTTGCCCTCGGCCTCGGCGCC 242988

RESULT 57 AC118963/c

8 8

51 GlyAlaGlyLeuProSerAlaSerAlaAla 60

US-09-989-890-238 (1-212) x SC0939120 (1-248550)

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REFERENCE
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RECEIVED STATES A GILLSONGOIGE GRADE DEATH WORKING DEAT SEQUENCE.
RECEIVED STATES A GILLSONGOIGE GRADE STATES TO SECURE A GILLSONGE GRADE STATES A GILLSONGOIGE GRADE STATES AND A GILLSONGOIGE GRADE GRADE STATES AND A GILLSONGOIGE GRADE GRADE STATES AND A GILLSONGOIGE GRADE GRADE
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                                                                                                                                                  AUTHORS
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Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23269749.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of loontigs daps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 249406: contig of 249406 bp in length.
Location/Qualifiers
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Mismatches:
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Center: Baylor College of Medicine
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Matches:
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/note="wgs_contig"
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Rattue norvegicus (Norway zet).

Rattue norvegicus (Norway zet).
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243241 CCATCCAGCTTAGCTCTTCTCTCCCAGACCC 243212
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                                                                                                                      DEFINITION
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                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                               RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrarty. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
    genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                    Center Clohe name: CH230-unknown
------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 206091 bases at least Q40
Consensus quality: 217431 bases at least Q30
Consensus quality: 217431 bases at least Q30
Estimated insert size: 219136; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
        shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
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2502 32601: gap of unknown length

2602 44171: contig of 11570 bp in length

44772 44271: gap of unknown length

4772 245205: contig of 200934 bp in length

5206 245305: gap of unknown length

6552 247051: gap of unknown length

6552 247051: gap of unknown length

6652 248359: contig of 1308 bp in length

660 251483: contig of 3024 bp in length

660 251483: contig of 3104 bp in length

660 251683: contig of 3104 bp in length
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                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                Center: Baylor College of Medicine
Center code: BCM
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mol_type="genomic DNA"
db_xref="taxon:10116"
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/estimated_length=unknown
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                                                                                                                                                                                   Center project name: KZL1
                                                               ----- Genome Center
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44172
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245306
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247052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
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25 ProSerSerLeuAlaLeuLeuSerArgPro 34

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Schizoparani, Murcoleas, Muridaes, Murinaes, Rattus.

Kobases I to 2556017.

Ruany, D.M., Adama, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Alabrocks S.L., Amaretunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bluage, K., Blankenburg, K., Bonnin, D., Budar, C., Burch, P., Burkett, C., Burchl, R., Drayd, N.C., Carron, T. B., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chan, G., Chen, R., Chen, R., Chowland, J., Christopoulos, C., Chen, R., Chen, R., Chen, C., Coyle, M.D., Dathorne, S.R., David, R., Delandy, K.R., Delagar, D., Edward, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delandy, K.R., Delagar, D., Edward, C.C., Elbaj, C., Barcht, D., M., Delaney, K.R., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edward, C.C., Elbaj, C., Bacotto, M., Ferraguto, D., Flagg, N., Fore, P., Prantz, P., Garrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Harrandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Harrandez, C., Harris, K., Harr, M., Havilak, P., Hawes, A., Harnandez, J., Howard, S., Hube, J., Hally, S., Hume, J., Jackson, L.E., Jackboon, B., Jia, Y., Johnson, R., Jollivet, S., Joudah, S., Mattins, B., Harring, R., Martins, M., Mayon, M., Mogue, M., Mohabet, W., Mattinay, R., Mattina, R., Wally, R., Mattina, R., Wally, R., Stoche, R., Mattina, R., Wally, R., Mattina, R., Wally, R., Mattina, R., Wally, R., Wally, R., Mattina, R., Wally, R., Wally
                 DNA linear HTG 13-NOV-2002
*** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA COLLEGE OF Medicine, One On Nov 13, 2002 this sequence version replaced gi:23267435.

The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                               Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                     AC126312.4 GI:24941465
HTG, HTGS PHASB1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
256017 bp
Rattus norvegicus clone CH230-1B9,
3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baylor Plaza, Houston,
3 (bases 1 to 256017)
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Unpublished
2 (bases 1 to 256017)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Schuegaganthi, Muroades, Murinas, Martins, Rattus,
Statueganthi, Muroades, Murinas, Martins,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.
Angalebechi, V., Aoyadi, A., Ayodeli, M., Bacas, E., Baden, H.,
Baldarin, D., Bandarmanike, D., Barder, M., Barnatead, M., Benahmed, F.,
Baldarin, D., Bandarmanike, D., Barder, M., Barnatead, M., Benahmed, F.,
Baldarin, D., Bandarmanike, D., Barder, M., Barnatead, M., Benahmed, F.,
Baldarin, M., Blair, J., Blair, Cassas, H., Center, A.,
Cardena, W., Carter, K., Cavaco, I., Caple, M., Cree, A., Chu, J.,
Claveland, C., Caverell, R., Cox, C., Coyle, M., Cree, A., Chu, J.,
Cardena, M., Carter, K., Cavaco, I., Coyle, M., Cree, A., Chu, J.,
Claveland, C., Caverell, R., Cox, C., Coyle, M., Cree, A., Chou, J.,
Claveland, C., Caverell, R., Cox, C., Coyle, M., Cree, A., Chu, J.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Egan, A., Becotto, M., Bugene, C., Fvans, C.A., Falls, T., Fand, G.,
Fraser, C., M., Ganla, R., Faldgy, M., Gurber, P.,
Fraser, C., M., Ganla, R., Flagg, M., Gurber, M., Forber, M.,
Gumarathe, P., Haland, M., Hamilton, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Harvey, Y., Havlak, P., Martin, R., Martin, R., Martin, M., Malloy, K., Marden, M.,
Jacob, L., Jang, H., Jang, H., Johnson, B., Johnson, R., Johlson, R.,
Johnson, B., Mayus, P., Martin, K., Martin, R., Martin, K., Mangum, A.,
Mangum, B., Mapus, P., Martin, K., Martin, R., Martin, K., Mangum, A.,
Mangum, B., Mapus, P., Martin, K., Martin, R., Martin, S., Mangun, S., Mclasch, M., Partin, R., Martin, S., Mangun, S., Mclasch, M., Perez, M., Perez, L., Petankoch, C.,
Partong, M., Quiroz, J., Rachlin, E., Reves, K., Regier, R., Roidester, B., Marten, J., Warten, R., Warten, R., Wall, S., Raigh, R.,
Sanders, W., Strong, R., Parton, M., Watzen, R., Walles, R., Weiss, R., Weiss
                                                                                                                                                                                                                                                                                                                                        J46316 bp DNA linear HTG 22-SEP-2002 ***, 11 unordered pieces.
AC107549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC107549.4 GI:23268118
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                    000
                                                                                                                                                                                                                      155464 GCTGCAGGGATTGCCTCCAGCGCTGTGGAG 155435
                 Mismatches:
Indels:
                                                                                                                                                                                         60 AlaAlaGlyIleAlaSerSerAlaValGlu 69
                                                                                                                                US-09-989-890-238 (1-212) x AC126312 (1-256017)
                 100.0%
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                       RESULT 60
AC107549
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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        and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

*NOTE: This is a "working draft" sequence. It currently

* Consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: TUNG
Center clone name: CH30-1B9
------- Summary Statistics
Consembly program: Phrap; version 0.990329
Consensus quality: 214827 bases at least Q40
Consensus quality: 219116 bases at least Q30
Consensus quality: 221911 bases at least Q30
Bstimated insert size: 222841; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 83721: contig of 83721 bp in length 22 83821: gap of unknown length 22 25367: contig of 16746 bp in length 8 25367: gap of unknown length 8 256017: contig of 2350 bp in length 1. cation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256017
10
0
                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /estimated length=unknown
83822. .85574
/note="wgs contig"
219978. .221353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-1B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end_sequence:BH274997"
38358. .39527
/note="wgs_contig"
67950. .69005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6668. .7475
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="wgs_contig"
78781. .81213
/note="wgs_contig"
83722. .83821
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253568. .253667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.02e+03
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100.0$
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83822
253568
253668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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db_xref="taxon:10116"

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Okamoto, H
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                                                    misc_feature
                                                                                                                              misc_feature
                                                                                                                                                                                                                                                        misc_feature
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu

Contact: pgc-help@bcm.tmc.edu

Center project name: GLDB

Center clone name: GLDB

Center clone name: GH30-45E20

Center clone name: GH30-45E20

Consensus quality: 188416 bases at least Q40

Consensus quality: 198446 bases at least Q30

Consensus quality: 196389 bases at least Q20

Consensus quality: 196389 bases at least Q20

Consensus quality: 196389 bases at least Q20

Consensus quality: 100 Bases; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of il contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                     Submitted (12-5EP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 22, 2002 this sequence version replaced gi:21731862.
The sequence in this assembly is a combination of BAC based reads and whole genome shocqun sequencing reads assembled using Atlas (http://www.ngsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigg that consist entirely of whole genome shocqun sequence reads. Both end sequences and whole genome shocqun sequence only contigs will be indicated in the feature table.
                                                                                                                      Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 1 Dases 1 to 346316) Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225315: contig of 225315 bp in length 225415: gap of unknown length 246434: gap of unknown length 246534: gap of unknown length 310670: contig of 64136 bp in length 31070: gap of unknown length 31238: gap of unknown length 312414: contig of 1268 bp in length 314414: contig of 2276 bp in length 314514: gap of unknown length 315550: contig of 1036 bp in length 315550: contig of 1036 bp in length 315550: contig of 10769 bp in length 31737: contig of 10769 bp in length 31737: contig of 10769 bp in length 31286: gap of unknown length 328286: gap of unknown length 33293: contig of 4667 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
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                          Unpublished
2 (bases 1 to 346316)
Worley, K.C.
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/organism="Rattus norvegicus" /mol_type="genomic DNA"

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Okamoto, H., Fukuda, M., Tawara, A., Nishizawa, T., Itoh, Y.,
Hayasaka, I., Tsuda, F., Tanaka, T., Miyakawa, Y. and Mayumi, M.
Species-specific TT viruses and cross-species infection in nonhuman
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Submitted (10-SEP-1999) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; 3311-1 Yakushiji, Minamikawachi-machi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TT virus DNA, untranslated region, isolate:Mf-TTV5
AB032303
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Mismatches:
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315551. .315650
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317318. .317417
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246435. .246534
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310671. .310770
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/estimated_length=unknown
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clone_end:Sp6
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Torque teno virus
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PRI 02-DEC-1997
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Anopheles gambiae cytochrome P450 (CYP49A1) mRNA, partial cds.
                                                                                                                                                                                                                                                                    Gizatullin,R.Z., Kashuba,V.I., Protopopov,A.I. and Zabarovsky,E.R. Unpublished 2 (bases 1 to 140)
Zabarovsky,E.R.
                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ranson, H. and Nikou, D.
Direct Submission
Submitted (19-SEP-2004) Vector Research, Liverpool School of
Tropical Medicine, Pembroke Place, Liverpool, Merseyside L3 SQA,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (18-APR-1997) Zabarovsky B.R., Karolinska Institute,
Microbiology and Tumorbiology Center, P.O. Box 280, Stockholm,
8-171 77, Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Boybera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
I (bases 1 to 303)
Ranson, H. and Nikou, D.
Cytochrome P450s from the malaria vector, Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCH903.1"
                                                                            140 bp DNA linear
H.sapiens genomic DNA fragment (clone NRLA100R).
295374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NRL NotI linking library"
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| /note="sequence surrounding NotI site"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 ProProProAlaAlaCysSerGlyAsp 45
 45 TCGTCACTGGCGCTCCTCCCCGACCT 19
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son, H. and Nikou, D.
                                                                                                                                     Z95374.1 GI:2661928
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HSZ95374/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRL 25-JAN-2000
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Submitted (10-SEP-1999) Hiroaki Okamoto, Jichi Medical School,
Submitted (10-SEP-1999) Hiroaki Okamoto, Jichi Medical School,
Immunology Division; 3311-1 Yakushiji, Minamikawachi-machi,
Kawachi-gun, Tochigi 229-0498, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:81-285-58-7404, Par:81-285-44-1557)
Location/Qualifiers
Kawachi-gun, Tochigi 329-0498, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:81-285-58-7404, Pax:81-285-44-1557)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolate:Mf-TTV6
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1. _100
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1. 7100
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/organiam="Torque teno virus"
/mol type="genomic DNA"
/isolate="Mf-TTV6"
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/note="untranglated region"
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Torque teno virus
Viruses; ssDNA viruses; Anellovirus.
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10627523
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RESULT 62 AB032304/c

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REPERENCE AUTHORS

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Score:

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Pred. No.:

Score:

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The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next ten bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 bp DNA linear STS 30-JUN-2004
MARC3174-3175 Bovine white blood cells Bos taurus STS genomic,
General Engled Site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Peocora; Bovidae; Bovinae; Bos.

1 (bases 1 to 354)
Stone,R.T.; Grosse,W.M., Casas,E., Smith,T.P., Keele,J.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of bovine EST data and human genomic sequences to map 100 gene-specific bovine markers
Mamm. Genome 13 (4), 211-215 (2002)
                                                                                                                                                       1. .340
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/clone lib="RTS-1"
/dev grage="adult"
/note="taurus and indicus crossbreds"
<1. .>340
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USDA/ARS U.S. Meat Animal Research Center
Box 166, Spur 18d, Clay Center, NE 68933, USA
Email: maith@email.marc.usda.gov
Primer A: GCCTGTACATCTGGACTTTCG
Primer B: TCCAGTGAGTAGGTGACCCC
                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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each 100 uM
0.25 units
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 minutes 95 degrees 30 seconds 95 degrees 30 seconds 58 degrees 2 minutes 68 degrees
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 GlyCysGlySerGlyAlaGlyLeuPro 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 GGTTGCGGTAGTGGTGCAGGTCTTCCA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-989-890-238 (1-212) x BV106213 (1-340)
                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G67666.1 GI:12802954
                                                                                                                                                                                                                                                                                                                                                         62.1
9.00
100.0%
100.0%
4.2%
                                                                                                                               electrophoresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taq Polymerase:
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Extension:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR Profile:
Hotstart:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denature:
                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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G67666/c
LOCUS
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COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                       STS
                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                               Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                             /product="cytochrome P450"
/protein id="AAU93487.1"
/b_xref="dI:5376655"
/translation="PPHLVVSNLQOYPEPDRRVPERWLKRGELKEHSGCPHAGQKIH
PYVSLPPGYGRRTCIGRRFAECELQILLSKLPRRYQVEYNYEKLTYKVNPTYIPDKP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340 bp DNA linear STS 05-MAR-2004
WARC 3319-3520:996679156:1 RTS-1 BOB indicus x Bos taurus STS
genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 340)
Snelling, W.M., Casas, E., Stone, R.T., Smith, T.P.L., Keele, J.W. and Bennett, G.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buffer:
Commercially supplied Qiagen HotStar buffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-50 ng genomic DNA
each 0.4 uM
each 100 uM
0.25 units (Qiagen HotStar)
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95 degrees for 30 seconds
58 degrees for 30 seconds
68 degrees for 1 minute
32 to 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Stone RT
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4166
Fax: 402 762 4173
Email: stone@email.marc.usda.gov
Primer A: AGATGTTTCTTAACACGCTGGA
                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos indicus x Bos taurus (hybrid cattle)
Bos indicus x Bos taurus
   /organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-989-890-238 (1-212) x AY745220 (1-303)
                                                        /dev_stage="larvae'
<1. .>303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Linkage mapping bovine ESTs
Unpublished (2004)
                                                                                                                            'gene="CYP49A1"
                                                                                         /gene="CYP49A1"
                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BV106213.1 GI:45184162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taq Polymerase:
                                                                                                                                                                                                                                                                                                      56.2
9.00
100.0%
100.0%
                                                                                                          <1. .>303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denature:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Template:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STS size: 500
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cycles:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protoco
                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BV106213/c
                                                                                                                                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                              gene
                                                                                                             CDS
                                                                                                                                                                                                                                                    ORIGIN
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8

PEATURES

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The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next ten bases averaged a quality score of 20 or greater. Amplicon size was estimated by agarose gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BV104270 379 bp DNA linear STS 05-MAR-2004
MARC 3198-3199:966881434:1 RTS-1 Bos indicus x Bos taurus STS
genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos indicus x Bos taurus (hybrid cattle)
Bos indicus x Bos taurus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bummalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bos.
I (basea I to 379)
Snelling,W.M., Casas,B., Stone,R.T., Smith,T.P.L., Keele,J.W. and
Bennett,G.L.
              Commercially supplied Qiagen HotStar buffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4166
Fax: 402 762 4173
Email: stone@email.marc.usda.gov
Primer A: ACAAGAAGACGATGCAGG
Primer A: ACAAGAAGACCATCTCGATCA
STS size: 500
PCR Profile:
Hotstart: 95 degrees for 15 minutes
                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/note="taurus and indicus crossbreds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos indicus x Bos taurus"
/mol type="genomic DNA"
/db xref="taxon:30522"
/clore_lib="RTS-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 degrees for 15 minutes
95 degrees for 30 seconds
58 degrees for 30 seconds
68 degrees for 1 minute
32 to 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                             <1. .353
complement (334. .353)
                                                                                                                                                                                              electrophoresis.
Location/Qualifiers
1. .354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linkage mapping bovine ESTs Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BV104270.1 GI:45182188
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9.00
100.0%
100.0%
4.2%
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Extension:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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                                                                                                                                                                                                                   FEATURES
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                                                                                                                                   1. :354.
Corganism="Bos taurus"
/mol_type="genomic DNA"
/db xref="taxon:9913"
/clone_lib="Bovine white blood cells"
/dev_stage="adult"
/noce="PCR amplification product from genomic DNA isolated from bovine WBC, Mixed breed crosses."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 bp DNA linear STS 05-WAR-2004
MARC 3174-3175:966894323:1 RTS-1 Bos indicus x Bos taurus STS
genomic, sequence tagged site.
                                 The STS sequence represents a contig of the sequences derived from each end using the amplification primers to sequence. The sequence does not represent the entire amplicon, as sequence close to the primers was of low quality.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos indicus x Bos taurus (hybrid cattle)
Bos indicus x Bos taurus
Bukaryota, Metazos, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 354)
Snelling, W.M., Casas, E., Stone, R.T., Smith, T.P.L., Keele, J.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Template: 25-50 ng genomic DNA
Primer: each 0.4 uM
dNTPs: each 100 uM
Tag Polymerase: 0.25 units (Qiagen HotStar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Stone RT
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4176
Fax: 402 762 4173
Email: stone@email.marc.usda.gov
Primer A: GCCTGTACATCTGGACTTTCG
Primer B: TCCAGTGAGTAGTGACCC
STS size: 400
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                    5 degrees for 15 minutes
5 degrees for 30 seconds
6 degrees for 30 seconds
8 degrees for 1 minute
2 to 45
Commercially supplied Qiagen HotStar buffer
                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 GlyCysGlySerGlyAlaGlyLeuPro 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 gerrecegragregrecaegrerreca 31
                                                                                                                                                                                                                                                                                                    <1. .353
complement (334. .353)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-989-890-238 (1-212) x G67666 (1-354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linkage mapping bovine ESTs
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BV104173.1 GI:45182089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
9
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9.00
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100.0%
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Cycles:
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Denature:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anneal:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bennett, G.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protocol
                                                                                                                                                                                                                                                                                                    primer_bind
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

RESULT 67 BV104173/c

ઠ

DEFINITION

ACCESSION

Query Match:

Pred. No.:

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/translation="IGKELAYDTARGOVDRLATALGROWTKGBAKKWGNAIESATGTTS
GDELSKKVCCKGTTSGSTNQCGVNATSGSTNNGKLSTVFNTDGAEAISSMDTTASGTS
STISLQGMAGNINSLTKDEKAIVAGAF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DM190E7T 442 bp DNA linear STS 06-MAY-1998
Drosophila melanogaster STS determined from European Mapping
Project cosmid, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institute of Molecular Biology and Biotechnology / Fo.R.T.H., P.O. 2 (bases 1 to 442)
Ashburner, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Exeryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.

1 (bases 1 to 442)
Papagiannakis,G., Spanos,L., Cox,S., Siden-Kiamos,I. and Louis,C. Sequencing the distal X chromosome of Drosophila melanogaster
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submission
Submission
Submission
Submission
Direct (29-APR-1998) Michael Ashburner, EMBL Outstation - The
EBL, Hinxton, Cambridge, CB10 1SD, U.K. E-mail:
ashburner@ebi.ac.uk. On behalf of the Buropean Drosophila Genome
Sequencing Consortium. For further information see the European
Drosophila Genome Sequencing Consortium's web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://edgp.ebi.ac.uk/
European Drosophila Genome Sequencing Consortium
STS_name = Dm190E7T
clone_name = 190E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442
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/mol type="genomic DNA"
/strain="Oregon-R"
/db xref="taxon:7227"
/clone="190E7"
                                                                      /product="major surface protein 2"
/protein id="AAAM89963.1"
/db_xref="G1:22037253"
                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                   171 ProLeuProValValLeuValAlaPro 179
                                                                                                                                                                                                                                                                                                                                                                                                                                          287 CCACTGCCAGTGGTACTAGTAGCACCA 313
                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                            (1-387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STS_from_promoter = T7
vector_class = cosmid, Lorist 6
origino_clone = Oregon_R
in_situ_site_primary = IE.
Location/Qualifiers
                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                              US-09-989-890-238 (1-212) x AF402268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL023365.1 GI:3123417
STS.
                   note="MSP2"
                                                                                                                                                                                                                                           69.3
9.00
100.0%
100.0%
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                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                      The STS is derived from PCR amplicons generated from genomic DNA, sequenced from each end using the amplification primers. The sequence does not necessarily represent the entire amplicon. Sequence derived from PolyPhred was trimmed from each end of each unique contig until five consecutive bases exceeded a quality score threshold of 20, and the next ten bases averaged a quality score electrophoresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCT 10-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anaplasma marginale expression site variant 196R-D major surface protein 2 (msp2) gene, partial cds.
AF402268
AF402268.1 GI:22037252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [bases 1 to 387]
Brayton, K.A., Palmer, G.H., Lundgren, A., Yi, J. and Barbet, A.F. Direct Submission
Submitted (25-UUL-2001) Veterinary Microbiology and Pathology, Washington State University, Pullman, WA 99164-7040, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anaplasma marginale str. Florida
Anaplasma marginale str. Florida
Bacteria, Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Anaplasma.

1 (bases 1 to 387)
Brayton, K.A., Palmer, G.H., Lundgren, A., Yi,J. and Barbet, A.F.
Antigenic variation of Anaplasma marginale msp2 occurs by
Combinatorial gene conversion
Mol. Microbiol. 43 (5), 1151-1159 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Anaplasma marginale str. Florida"
/mol_type="genomic DNA"
/strain="Florida"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolate="expression site variant 196R-D"
/db xref="taxon:320483"
<1. .>387
Primer: each 0.4 uM
dNTPs: each 100 uM
Tag Polymerase: 0.25 units (Qiagen HotStar)
                                                                                           Commercially supplied Qiagen HotStar buffer
                                                                                                                                                                                                                                                                                                                                                                                             /dev stage="adult"
/note="taurus and indicus crossbreds"
<1. .>379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Bos indicus x Bos taurus"

mol type="genomic DNA"

db xref="taxon:30522"

clone_lib="RTS-1"
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                                                                                                                                                                                                                                                                          Location/Qualifiers
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<1. .>387
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AF402268
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BV308315.1 GI:57506807
                                                                              Canis familiaris (dog)
                                                                                                                                                          1 (bases 1 to 501)
Lindblad-Toh, K.
                                                                                                Canis familiaris
                                                                                                                                                                                                                                                                                                        Tel: 6172521477
Fax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                          STS size: 501
                                                                                                                                               Canis.
                                                VERSION
KEYWORDS
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                                                                                                                                                                                     Drosophila melanogaster STS determined from Buropean Mapping Project cosmid, sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institute of Molecular Biology and Biotechnology / FO.R.T.H., P.O. Box 1527, GR-711 10 Heraklion, Crete, Greece.

2 (Dases 1 to 453)
Ashburner, M.
Direct Submission
Submitted (29-APR-1998) Michael Ashburner, EMBL Outstation - The BEL Hinkton, Gambridge, CB10 185, U.K. E.mail:
ashburner@ebi.ac.uk. On behalf of the European Drosophila Genome Sequencing Consortium. For further information see the European Drosophila Genome Sequencing Consortium's web site:
                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 453)
Espagiannakis,G., Spanos,L., Cox,S., Siden-Kiamos,I. and Louis,C. Sequencing the distal X chromosome of Drosophila melanogaster Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://edgp.ebi.ac.uk/
Buropean Drosophila Genome Sequencing Consortium
STS_name = Dms6A7T
clone = name = 96A7
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                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
                                                                                                            CTACCATCCGCCAGCGCCGCCGCCGGN 272
                                                Gaps:
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/strain="Oregon-R"
/db_xref="taxon:7227"
/clone="96A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuProSerAlaSerAlaAlaAlaGly 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector_class = cosmid, Lorist 6
origin of clone = Oregon_R
in_situ_site_secondary = 3C
in_situ_repetitive number = >40.
Location/Qualifiers
                                                                               US-09-989-890-238 (1-212) x DM190E7T (1-442)
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BV308315/c
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BV345691 604 bp DNA linear STS 27-JAN-2005 S230P6315FF6.TO Rottweiler Canis familiaris STS genomic, sequence tagged site.
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ni,J., Young,P., Rosen,C.A., Florence,K.A., Ruben,S.M.,
Carter,K.C., Feng,P., Endress,G.A., LaFleur,D.W., Shi,Y., Janat,F.,
Duane,D.R., Greene,J.M., Ferrie,A.M. and Yu,G.L.
Novel secreted protein
Patent: EP 1445116-A 73 11-AUG-2004;
Patent: EP 1445116-A 73 11-AUG-2004;
Human Genome Sciences, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 PAT 19-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Lindblad-Toh.K.
The genome sequence of Canis familiaris
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                      DNA

    .546
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                 CQ849043 546 bp
Sequence 73 from Patent EP1445316.
CQ849043
                                                                                                                                                                                                                            US-09-989-890-238 (1-212) x CQ849043 (1-546)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CQ849043.1 GI:51470455
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BV345691.1 GI:57599570
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Canis familiaris
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                       93.2
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A61P43/00,C07K14/47,C07K16/00,C12N5/10,C12P21/02,C12Q1/68, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PI JOHN M GREENE, PAUL YOUNG, ANN M FERRIE, GUO
LIANG YU, FOUAD JANAT,
LI JIAN NI,
PI KENNETH, C CARTER, GREGORY A ENDRESS, PING FENG, DAVID W LAFLEUR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C12N15/09, A61K31/711, A61K38/00, A61K48/00, A61P25/00, A61P35/00,
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1 (Base 1 to 546)

Duan, R.D., Plorence, K.A., Rosen, C.A., Ruben, S.M., Greene, J.M., Young, P., Ferrie, A.M., Yu, G.L., Janat, F., Ni, J., Carter, K.C., Endress, G.A., Feng, P., Lafleur, D.W. and Shi, Y.

101 human secretory proteins
Patent: JP 2001519156-A 72 23-OCT-2001;

HUMAN GENOME SCIENCES INC
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PD 23-007-2001
PD 23-007-2001
PD 01-007-1998 JP 2000515006
PD 02-007-1997 US 60/060837,02-007-1997 US 60/060862 PR 02-007-1997 US 60/060845,02-007-1997 US 60/060846, PR 02-007-1997 US 60/060838,02-007-1997 US 60/060838, PR 02-007-1997 US 60/060838, PR 02-007-1997 US 60/060838 PR 02-007-1997 US 60/06083 PR 02-007-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC G01N33/53,G01N33/566,C12N15/00,C12N5/10,C12P21/02,C12(human secretory proteins
FH Key
FT Source
Tocation/Qualification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ce 1. .546 /organism='Homo sapiens (human)'. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
/strain="AlaskanMalamute"
|db.xref="taxon:9615"
|map="+ 23 26-445 55235003-55234584"
|Clone 1lb="AlaskanMalamute"
<1...>501
                                                                                                                                                                                    501
0
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0
                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                 US-09-989-890-238 (1-212) x BV308315 (1-501)
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JP 2001519156-A/72.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                    86.5
9.00
100.0%
100.0%
4.2%
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Best Local Similarity:
Query Match:
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PAT 05-MAY-2005

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AY150443

AY150443.1 GI:23297512

AY150443.1 GI:23297512

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II: Brassicales; Brassicaceae, Arabidopsis.

B 1 (bases 1 to 1210)

S Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,

Quach,H.L., Tang,C.C., Torlumi,M., Wallender, B.K., Wong,C.,

Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J.,

Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T.,

Arabidopsis Open Reading Frame (ORF) Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY150443 1210 bp mRNA linear PLN 23-SEP-2002
Arabidopsis thaliana unknown protein (At1g51560) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
Quach,H.L., Tang,C.C., Toriumi,M., Wallender,B.K., Wong,C.,
Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J.,
Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T.,
Davish,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Tuereci,O., Sahin,U., Helftenbein,G. and Schlueter,V. Identification of tumour-associated cell surface antigens for diagnosis and therapy
Patent: WO 20050302560-A 69 07-APR-2005;
Ganymed Pharmaceuticals AG (DE)
Location/Qualifiers
                                                                                                                                                                 linear
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Matches:
Conservative:
Mismatches:
                                                                                                                                                     Sequence 69 from Patent WO2005030250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                        31 LeuSerArgProLeuSerProProPro 39
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                                                                                                                                                                                                                                CS074643.1 GI:63091233
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                                                                                                                                                                                                                                                                            Homo sapiens (human)
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annotated with alleles from the boxer and the breed or canid from
which the particular
read came. The validation rate for these SNPs was estimated at
approximately 98%.

WGA-discovery (WGA) of Boxer/Poodle SNPs:

A second set of SNPs was generated using a similar methodology
except that the contigs
from the 1.5x poodle assembly (Kirkness 2003) were used instead of
wGS reads. Since this
sequence lacked base quality scores, arbitrary quality scores of
phred 40 were assigned base quality scores, arbitrary quality scores of
boxer assigned base quality scores, arbitrary quality scores of
boxer assigned out by SSAHA-SNP. 1637780 SNPs were annotated
with alleles from the
boxer and the poodle. The validation rate for these SNPs was
estimated at approximately TBD%.

Internal-WGA-discovery (I-WGA):

A third set of SNPs were discovered by comparing reads in the WGA
assembly. SNPs were
defined as mismatch positions that had a base quality of >= 30 on
both reads in a region
that allgned without gaps, and with at most one additional mismatch
in the ren flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the ten flanking bases. For each allele, at least one additional read had to confirm
it. 731476 SNPs were
                                                                                                                                                                                                                                                                                   German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador Retriever, English Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese Water Dog -100,000 each) and five other canids (Chinese, Alaskan, Indian and Spanish Gray Wolf as well as the Californian Coyote).

The WGS reads were placed uniquely on the CanFaml.0 boxer assembly and SNP detection was carried out by SSAHA-SNP. 863872 reads were annotated as STSs and 485941 SNPs were
                                                                                                                                                                                                        Protocol:
WGS-discovery (WGS):
Paired-end low-coverage whole genome shotgun reads were generated
from 9 breeds
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotated with alleles between the two boxer alleles. The validation rate for these SNPs was estimated at approximately TBD%.

Location/Qualifiers
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/map="+ 11 22-543 12395351-12394828"
/clone_lib="Rottweiler"
/-1. .>604
                                             320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="Rottweiler"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                 Tel: 6172521477

Fax: 6172580903

Email: kersli@genome.wi.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-989-890-238 (1-212) x BV345691 (1-604)
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Pred. No.:

Score:

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AY188374
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THE GEWSCLSRARVTLEGDVYPPLDEBQDWAHKQVRAKHQGSPGQWGRHFFRWQNISD
IYPTGGFGYVAMINYBYETLQPPKAVMGGSQNLKELMAIFSKPLRELLSSENELDD
AAIISIDSKGIDIRVRQGAQPKIQRLAFEESHGVETLEEAKSALWKVIEKGKLHNLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AY508007 1301 bp mRNA linear PLN 01-JAN-2005 Helianthus annuus DREB2 transcription factor (DREB2) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                          /translation="MDAAIFTSVYVCNIPKTKKAFFNPNPPALSSSSCWLCNSQAKQI
IKLRIREGSNQGLLRVHALFNNEEASSESEDKNGFGLLPADIPSLPQEKFGSNVSGEK
DSENIIDVETSLAVPHGGGTRAGLFRTPISGGVQSATSAHGLPRPALAVRNLMEQARF
Street, Albany, CA 94710, USA
Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.
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Jac-Martin, J., Almoguera, C. and Jordano, J.

A specific interaction between HaDREB2 and HaHSFA9 mediates transcriptional activation during embryo desiccation in sunflower Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1301)
Diaz-Martin,J., Almoguera,C. and Jordano,J.
Direct Submission
Submitted (17-DEC-2003) Biologia Vegetal, IRNAS (CSIC), Av. Reina Mercedes, 10. Apartado 1052, Sevilla 41080, Spain
Location/Qualifiers
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9
0
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                                                                                                                                                                                'ecotype="Columbia"
'note="This clone is in pUNI 51."
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                             thaliana"
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                                                                                                                                                                                                                                                                                                                         /product="unknown protein"
/protein_id="AAN12985.1"
/db_xref="GI:23297513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-1210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
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/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                       evidence=experimental
                                                                                                                                                                                                                                                                       gene="At1g51560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1180. .1210
/gene="At1g51560"
                                                                                                                                                                                                                                   /gene="At1g51560"
                                                                                                                                                  chromosome="1"
clone="C104814"
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AY508007.1 GI:46241281
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JOURNAL
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/note="class A2 DREB transcription factor from the plant AP2/ERF family; invoved in the developmental regulation of small heat shock protein (SHSP) genes in embryos; shows physical and specific genetic interaction with a second transcription factor HSFA9 encoded by GenBank Accession
                                                                                                                                                                                                                                                                                                                                                                                                     /codon start=1
/product="DREB2 transcription factor"
/product="DREB2 transcription factor"
/product="DREB2 transcription factor"
/protein_id="MAASQSB61.1"
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TNPASSCDSTTTCSYSVDATHDSKPGFAVENSPSVKHEESVQVKHEPEIVAKEHCVDN
NDLGFDIGDEMFDLEELLGAVEDSNPEAGSGDGYDGRFVNGADANENMOMYMQPDFCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLN 06-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="rich in acidic amino acids; required for functional
synergism with HSFA9; Region: transcription activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sporisorium sp. 0-058.1d
Sporisorium sp. 0-058.1d
Sukaryotas, Fungi; Basidiomycota, Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Sporisorium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sporisorium sp. 0-058.1d internal transcribed spacer 1, partial sequence; 5.85 ribosomal RNA, internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="DNA-binding domain; involved in protein-protein
Interaction with HSFA9; Region: AP2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nectar-Inhabiting Yeasts in Silene latifolia and Co-flowering
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                                                                       /db_xref="taxon:4232"
/dev_stage="developing embryo; 14 dpa"
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Golonka, A.M.
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organism="Helianthus annuus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=experimental
                     /mol_type="mRNA"
/cultivar="P113HS"
                                                                                                                                                                                                                                                                                                                                                                                Number AY099451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-989-890-238 (1-212) x AY508007
                                                                                                                                                                            'note="HaDREB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY188374.1 GI:28826190
                                                                                                                                                                                                      .68. .1112
/gene="DREB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435. .608
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Best Local Similarity:
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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E (bases 1 to 1362)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Colling, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopking, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, R. Brownstein, M.J., Usdin, F.B., Toshiyuki, S.,
Garninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Banchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Youngh, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Youngh, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalaka, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S. J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOTO 1317 1362 bp mRNA linear PRI 02-AUG-2005 Homo sapiens CDNA clone MGC:120420 IMAGE:40024858, complete cds. BC101317
                                                                                                                                                                                                                                                                                                          /isolation_source="nectar"
| Mb_xref="texon:220537"
| Anote="species | Or generic] identification based on nrDNA sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                           3 (bases 1 to 1327)
Golonka, A.M., Vilgalys, R. and Antonovics, J.
Direct Submission
Submitted (27-NOV-2002) Biology, Duke University, PO Box 90338,
Durham, NC 27708, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 26S ribosomal RNA"
Nectar-Inhabiting Yeasts in Silene latifolia and Co-flowering
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                                           Thesis (2002) Duke University, Durham, NC, USA
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|strain="0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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Query Match:
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BC101317
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
cDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MARQDLLDQVGGLGRRQILQMVFLIMFNVIVYHQTQLENFAAFI
LDHRCWVHILDNDTIPDNDPGTLSQDALLRISIPFDSNLRPEKCRRFVHPQWKLIHLN
GTPPRTSEPDTEPCVDGWVYDQSSFPSTIVTKVAGRVCSVAHYQQQTRRGLKGTYKSC
TQEWNEEC"
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                                                                        Direct Submission
Submitted (01-AUG-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
Series: IRAM Plate: 7 Row: n Column: 8.
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Goldman, B.S., Hinkle, G.J., Slater, S.C. and Wiegand, R.C. Myxococcus xanthus genome sequences and uses thereof Patent: US 683347-A 8319 21-DEC-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
product="Unknown (protein for MGC:120420)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Mismatches:
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Sequence 8319 from patent US 6833447.
AR626918
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1235 TTGCCATCCTCTGGCCTTGTTGTC 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAI01318.1"
db_xref="GI:71680580"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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(bases 1 to 1362)
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/tanslation="MDAT805"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHLCTVMSKMHHRREGYPFGSLVDFAPDPMGHPIFSFSPLAIHTRNIIJAEPRCTLVVVO
IPGMSCLSRAVTLEGDVYPLPERQGWAHKQYMKKHGGGSQOMGNHFYBRMQNISD
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AAIISIDSKCIDIRVRQGAQPKIQRLAFESSHGVETLEBAKSALMKVIEKGKLHNLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF153341 1448 bp DNA linear PRI 24-AUG-2001 Homo sapiens winged helix/forkhead transcription factor (HFH1)
                                        Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic sequence resulting in an amino
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                  'ecotype="Columbia"
'note="This clone is in a modified pBluescript vector
(PLC-1) as a BamHI/XhoI insert."
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Arabidopsis thaliana"
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1258..1436
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/gene="At2951560"
/gene="At1g51560"
/note="not in genomic sequence"
                                                                                                                                                                                                                                        clone="RAFL08-11-G16 (R11062)"
contributed equally to this work as PIs.
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acid sequence difference"
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gene="At1g51560"
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1 (bases 1 to 1448)
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1436)

S Yamada, K., Liu, S. X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K.,

Goldsmith, A. D., Lee, J. M., Quach, H. L., Toriumi, M., Yu, G., Bowser, L.,

Carninoi, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin, Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Shinn, P., Southwick, A., Shinozaki, K.,

Bavis, R. W., Ecker, J. R. and Theologis, A., Shinozaki, K.,

Arabidopsis Pull Length cDNA Clones

Luppblished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLN 18-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (ILJAN-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA): 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Mebuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY074356 1436 bp mRNA linear PLN 18-SEP-:
Arabidopsis thaliana unknown protein (At1g51560) mRNA, complete
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Matches:
Conservative:
Mismatches:
Monsanto Technology, LLC; St. Louis, MO
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1. .1377
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAF75586.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKPFRSRRLRDTAPGTTLQWGAAPCPPLPAFPALLPAAPCRALLPLGAYGAGEPARLG
AREAEVPPTAPPLLLAPLPAAAPAKPLRGPAAGGAHLYCPLRLPAALQAALVRRPGPH
LSYPVETLLA"
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                                                                                                    LOGAL TO 1448)
Hong H.-K. Noveroske, J.K., Justice, M.J. and Chakravarti, A. Hong H.-K. Noveroske, J.K., Justice, M.J. and Chakravarti, A. Briect Submission
Submitted (21-MAY-1999) Genetics, Case Western Reserve University, 10900 Euclid Avenue, Cleveland, OH 44106-4955, USA Location/Qualifiers
                                                                                                                                                                                                              1. 1448
| Organism="Homo sapiens"
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| Chromosome="6" |
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| 433. .>1441 |
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| product="Winged helix/forkhead transcription factor"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hong, H.K., Noveroske, J.K., Headon, D.J., Liu, T., Sy, M.S., Justice, M.J. and Chakravarri, A. The winged helix/forkhead transcription factor Foxql regulates differentiation of hair in satin mice Genesis 29 (4), 163-171 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon_start=1
|product="winged helix/forkhead transcription factor"
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AX685724
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/gene="HFH1"
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/ LTAIN 1 A LOID "MARQDLIDQVGGLGRFQILQMVFLIMFNVIVYHQTQLENFARFI
LDHRGWYHILDNDTI PDNDFGTLSQDALLER IS IPFOSINLRFBEKCRRFWHPQWKLIHLIN
LDHRGWYHILDNDTI PDNDFGTLSQDALLER IS IPFOSINLRFBEKCRRFWHPQWKLIHLIN
TENFWITSBPTBFCVGGWYDQSS PESTI VTKWDLVCESGPLNSVARFLFMAGWAWGG
NLYGHILSDRFGRKFLNRSYLQLA IVGTCAAFAPTILVYCSLIRFLAGAATFSI IVWT
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                                                                                                                                                                                                                                                                                                                                                                               PRI 12-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae, Homo.

1 (bases 1 to 1644)

1 starly, S.A., Monte,J.C. and Nigam,S.K.

Novel slc22 transporter homologs in fly, worm, and human clarify the phylogeny of organic anion and cation transporters

(er) Physiol. Genomics 18 (1), 12-24 (2004)
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Monte, J.C., Nigam, S.K. and Braly, S.A.
Direct Submission
Submisted (13-OCT-2003) Medicine, University of California, San
Diego, 9500 Gilman Drive, La Jolla, CA 92093-0693, USA
Location/Qualifiers
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/product="putative UST1-like organic anion transporter"
/protein id="AAR84082.1"
/db_xref="G1:40287955"
                                                                                                                                                                                                                                                                                                                                           1644 bp mRNA linear PRI 12-NOV-
Homo sapiens putative UST1-like organic anion transporter mRNA,
AX437532
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Mismatches:
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  Length:
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Indels:
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/organism="Homo_sapiens"
                                                                                                                                                                            US-09-989-890-238 (1-212) x AX685724 (1-1644)
                                                                                                                               Gaps:
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/lisuue_type="kidney"
1. .1644
/note="UST6"
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GRNELGEDAANFVLTYSGALLIKAENNTEMGTFPLEIAKGYENALSHTWEVLEETCADK
IETVESEKELIKAIFTCISSKQYGNEDFLSDLVAKAILTVLPKDPSKFNVDNIRVKI
MSSLINSGQVKGMYPRPREGYTYREKREAKVYNFSCPLDISGYGTKTGYTLLHNAQEM
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LCRVVGATPLARMGVPMPEEMGSVDVVETIEIGGDRVTVFRQVEDITRIATIVLRGAT
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QYGEAFEVVPRTISENAGLDPTDVISKLYAAHHKENGESIGVDVECENDGTLDAKEAG
IFDVLLAKKSAIRLATETVLTVLNVDQVVMSKPAGGPKPPGPNPHWDDD"
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,

    1676
    Interest of the supplex part of the supplex part of the supplex part of the supplex part of the subunit, SWISS-PROT Accession Number part of the subunit of
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                      /db xref="taxon:4896"
/clone="SY1780"
/clone_lib="library of H. Nojima"
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Patent: WO 0204250.6 I 17-JAN-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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/db_xref="GI:1749752"
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  strain="PR745
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Submitted (15-NOV-1996) Sachiyo Yoshioka, Tsukita Cell Axis Project
Submitted (15-NOV-1996) Sachiyo Yoshioka, Tsukita Cell Axis Project
ERATO UST, Kyoto Research Park; 17 Chudouji Minamimachi,
Shimokyo-ku, Kyoto, Kyoto 600, Japan
(E-mail:syoshi@cell:tsukita.jst.go.jp, Tel:+81-75-315-7913,
Fax:+81-75-315-6420)
Location/Qualifiers
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Yoshioka,S., Kato,K., Nakai,K., Okayama,H. and Nojima,H.
Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
Unclassified.
1 (bases 1 to 1716)
1 (bases 1 to 1716)
Goldman, B.S., Hinkle, G.J., Slater, S.C. and Wiegand, R.C. Myxococcus xanthus genome sequences and uses thereof Patent: US 6833447-A 9034 21-DEC-2004;
Monsanto Technology, LLC; St. Louis, MO
Location/Qualifiers
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Schizosaccharomycetales; Schizosaccharomycetaceae;
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/mol_type="mRNA"
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Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                       AR627633 1716 bp DNA
Sequence 9034 from patent US 6833447.
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                                                     US-09-989-890-238 (1-212) x AY437532 (1-1644)
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/mol_type="genomic DNA"
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PAT 31-MAR-2003

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Homo sapiens
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                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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Organic anion transporting (oat)-like protein ust3-likel and
                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                 Patent: WO 2004081041-A 1 23-SEP-2004;
                                                                                                                                                           Sequence 1 from Patent WO2004081041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transporters and ion channels
Patent: WO 0204250-A 62 IT-JAN-2002;
Incyte Genomics, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 62 from Patent W00204520.
AX687002
                                                                                            1685 TIGCCATCCTCTGGCCTIGTTGTCC 1711
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              Gaps:
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                                           US-09-989-890-238 (1-212) x AX687001 (1-1818)
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Location/Qualifiers
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Homo sapiens (human)
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Best Local Similarity:
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CQ876112
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TITLE
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Homo sapiens forkhead box Q1, mRNA (cDNA clone MGC:61699
IMAGE:6010412), complete cds.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgri.nih.gov
Contact: N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
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0 0 0
0 0 0
/organism="Homo sapiens"
|mol_trype="unassigned DNA"
|db_xref="taxon:9606"
|noTe="Incyte ID No: 7472734CB1"
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Mismatches:
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PLSRVGWRPVSRVALYKSVPTRLLSRAMGRLNQVELPHWLRRPVYSLYIWTFGVNMKE
AAVEDLHHYRNLSEFRRKKKPQARPVCGLHSVISPSDGKTLNFGVKRCEVEQVKGV
TYSLESFLEPRPRPPEPPPPATPHSSFRSQLYNTEGNELLYCIYILAPGDYCRCFHSP
TDWTVSHRRHPPGSLMSVNPGMARWIKELFCHNERVVLTGDWKHGFFSLTAVGATNVG
STRIYPSRDLHTNSPRSGYNDFSFYTHANKEGIPMRKGEHLGEFNLGSTIVLIFE
APKDFNFRLQAGQKIRFGEALGSL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab host="Escherichia coli DH108"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue From marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-MAR-2005) Molecular Genetic Research Unit, USDA-ARS
U.S. Meat Animal Research Center, P.O. Box 166, Spur 18D, Clay
Center, NB 68933
Contact: Gregory P. Harhay at harhay@email.marc.usda.gov.
Location/Qualifiers
1. 2386
/organis=Box taurus*
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/db_xref="taxon:9913"
Smith, T.P., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Haeton, M. Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                       Unpublished
3 (bases 1 to 2386)
Harhay,G.P., Sonstegard,T.S., Van Tassell,C.P., Clawson,M.L.,
Haeron,M.P., Keele,J.W., Snelling,W.M., Weidmann,R.T. and
Smith,T.P.L.
                                                                                                                                                                                                                          2 (bases 1 to 2386)
Harhay, G.P., Sonstegard, T.S., Van Tassell, C.P., Clawson, M.L.,
Heaton, M.P., Keele, J.W., Snelling, W.M., Weidmann, R.T. and
                                                                                                                                                                                                                                                                                                                         Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone=13BOV55119; plate 59 row I column 19"
/tissue type="pooled"
/clone lib="3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="phosphatidylserine decarboxylase"
protein id="AAX46472.1"
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                                                                                                                             TITLE
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                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 115 Row: i Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
                         Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masillo, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McClowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DCAANSPAAGGGARDPPGDGBQSAGGGPGAEEAIPAAAAAVVAEGAEAGAGFGAGG
AGSGBGARSKPYTRRPKPPYSYIALIAMAIRDSAGGRLFLAEINBYLMGKFPFRGSY
TGWRNSVRHNLSLNDCFVKVLRDPSRPWGKDNYWMLNPNSEYTFADGVFRRRRKRLSH
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LRKPFRSRRLRDTAPGTTLOWGAAPCPPLPAPPALLPAAPCRALLPLCAYGAGEPARL
GAREAEVPPTAPPLILAPLPAAAPAKPLRGPAAGGAHLYCPLRLPAALQAASVRRPGP
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Bos taurus phosphatidylserine decarboxylase (PISD), mRNA, complete
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
     Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.
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/ordanism="ROM"
/db tref="taxon:9606"
/clone="MGC:61699 IMAGE:6010412"
/tissue type="Lung, large cell carcinoma"
/clone libe="NH MGC_68"
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="synonym: HFH1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 AlaAlaAlaGlyIleAlaSerSerAla 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'lab host="DH10B'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BT021625
BT021625.1 GI:61553872
FLI_CDNA.
Bos_taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="FOXO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="FOXQ1"
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1.00.0%
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Best Local Similarity:
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ORGANISM
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KEYWORDS
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, M., Yazaki, J., Ishikawa, W., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Oohada, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group., Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kuroseki, T., Kodama, T., Maeuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariawa, R., Ishibiki, J., Kawamata, M., Yoshimura, S., Nikura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Watsubara, K., RikKishi, Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Arakawa, T., Pubuda, S., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshimo, M. and Hayashizaki, Y., Solinga, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                         VI OEKVPFNDŤOLSDYNSLNVPAHNRRHQLRAREVAAGALVFLQNLVSALLÅFHSYSE
CYTOLY PRISSIETI SAVNOKESQYLHENASYLRQLEBOLLOCHHGSTIFEDLPAATOKF
CYTORCLLSSLASILSSGGKWATFFSNSLDPLTSCAGSPSGALLKPLQADSYWOSKR
RAAAVISSYRQARAESVPYGRALANHILLTSSTESREGLMQOVLQSQOKISRLEOBKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HWLLEAQLAQVRLOKESARTAQLEAQVCVSAPQSQLCASAAESPVCVSAAESQVCVSA
AETPERPALADAPEPLQDTSVVGVLJE TRSCESESADQOSREQLIKTHYMSRVSELTYQ
LQTCDSKAVHFHAECRAVARKLAMAERSRDTLGEELKLANQNITRLQDELSTTRRSYE
DQLSMMSDHLCSMNETLSQQRETIDTLKLSAKGNAKKNKSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2576 bp mRNA linear PLN 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:J033004J13, full insert sequence.
                                                                                                                                                                                                                           /db_xref="ZFIN:ZDB-GENE-041114-8"
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                                                                                                                                                                                                                                                                                                                         ŌSVPDEDLHKKIQENERLHIQMLEAQECHQQQEAQLSSRLQOLQEEAQEHQAQLEELS
CRHAHTIHTLQEDKATLEVKLQTLEREARDCRVRTEECQQQLRKYQSEVSSQLKHSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK073176.1 GI:32983199
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Science 301 (5631), 376-379 (2003)
                                                                                                 /product="zgc:92087"
/protein_id="AAH85632.1"
/db_xref="GI:55250682"
                                                                                                                                                                               db_xref="GeneID:492333"
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100.0<del>$</del>
4.2$
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KEYWORDS
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                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Collins, E.S., Wagner, D., Shemmen, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hang, L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Norley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Marah, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Bauffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Bautterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome
CA 94305
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 55250681.
Location/Qualifiers
BC085632 2417 bp mRNA linear VRT 06-JUL-2005
Danio rerio 2gc:92087, mRNA (cDNA clone MGC:92087 IMAGE:7047030),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University Solution of Medicine, Stanford, CA 943:
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-NOV-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="MGC:92087 IMAGE:7047030"
/tissue_type="Whole, adult zebrafish"
/clone_lib="NIH_ZGC_10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="zgc:92087"
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Tissue Procurement: Len Zon, Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Danio rerio"
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/db_xref="taxon:7955"
                                                                                                                                BC085632.1 GI:55250681
                                                                                                                                                                                            Danio rerio (zebrafish)
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                                                                      complete cds.
                                                                                                                                                                                                                                  Danio rerio
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                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
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DEFINITION
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AUTHORS
CONSRTM
TITLE
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COMMENT
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TITLE

Conservative: Mismatches: Indels: Length: Matches:

Gaps:

PRI 12-JUN-1993

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LEGDQGVISSLLKDHTSGSKLTQLKTAQRLEDLDQPKLDEDTRRIKQGSPNGYAVLLAT
QATPSGLGTEGMPTVEPGLQRRLLENLVSYLKQXAGAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.

1 (bases 1 to 2893)
Shridhar, V., Kamat, A.K., Golembieski, W., Smith, S.E.,
Siegfried, J.M., Hunt, J.D., Miller, O.J., Wozniak, A. and Smith, D.I.
Identification of new genes from human chromosomal band 3P21.1 and
Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Homo sapiens adenogastric carcinoma, gastric mucosa cDNA to mRNA.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="adenogastric carcinoma, gastric mucosa"
1627. .7397
                                                                                                                                                                                    HUMAGCGB 2893 bp mRNA linear l
Human chromosome 3p21.1 gene sequence, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 2893
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                              199 CGCCGCTTTCTCCGCCACCGGCAGCC 225
            33 ArgProLeuSerProProProAlaAla 41
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                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                      L13434
L13434.1 GI:291843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
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DEFINITION
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VERSION
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VERSION
                                                                                                                               RESULT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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                                                                                                                                                                                                                                                                                                              KEYWORDS
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                                                                                                                                                              HUMAGCGB
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                                                                                                                                                                                                                                                                                                                                             SOURCE
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Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikada,R., Imamura,K., Imottani,K., Ishibiki,J., Ishikawa,M., Icoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kamamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodam,T., Kojima,Y., Kojima,Y., Kodam,Y., Komo,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Miura,J., Miyazaki,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,R., Muraka,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Oka,M., Ooka,H., Osato,N., Oteok,M., Osato,N., Osato,N., Sahai,C., Sakai,K., Sakai,M., Shinagawa,A., Shiraki,T., Shishiki,T., Satoh,K., Shibata,K., Shinaki,R., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami,Takeda,Y., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoco, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
FAIS Genome Sequencing & Analysis Group: N. Kobayashi, M.,
Kodama, T., Kursumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Fyu, R., Sugano, S.,
Sugiyama, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hizamoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Karch, H., Kawai, J.,
Kishikawa-Hirozane, T., Matsuyama, T., Miyazaki, A., Murata, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Namasaki, R., Ohno, M., Osato, N.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sagabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, Y., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mail-skikuchi@nias-affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="txon: 39947"
/clone="1033004113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2576
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Conservative:
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TITLE JOURNAL

COMMENT

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AK065775 3353 bp mRNA linear PLN 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:J013038N04, full insert sequence.
AK065775.1 GI:32975793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (jappnica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, viridiplantae; Streptophyra; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
2893
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                                                   Conservative:
                                                                    Mismatches:
Indels:
Length:
Matches:
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                                                                                                                          Gaps:
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SOURCE
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Mismatches: Indela:

Percent Similarity: Best Local Similarity: Query Match: DB:

Score:

FEATURES

ORIGIN

US-09-989-890-238 (1-212) x AK073176 (1-2576)

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UNEL: http://contaol.dna.airrc.go.jp/cuh.k.

Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,

Ishikawa,M., Yamada,H., Ooka,H., Hottel,T., Kojima,K., Namiki,T.,

Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and

YASIS Genome Sequencing & Analysis Group: Otomo,Y., Idda,Y.,

Pujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,

Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,

Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S.,

Sugiyama,A., Matsubara,K. and Murakami,K., Susika,R., Suzuki,Y., Tsuunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,

Yoshimura,A., Matsubara,K. and Murakami,K., Hanagaki,T.,

Akimura,T., Arakawa,T., Carninci,P., Pukuda,S., Hanagaki,T.,

Hara,A., Hashizume,W., Hayashida,K., Hayatau,M., Hiramoto,K.,

Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,

Kishikawa Hixozane,T., Nomura,K., Imamura,M., Imata,M.,

Kishikawa Hixozane,T., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,

Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,

Sasaki,D., Sato,K., Shibata,K., Sakazume,N., Sano,H.,

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Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahaqi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kurosaki, T., Kodama, T., Masuda, H., Kobaysahi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mazuno, K., Yokomizo, S., Mikura, J., Kawamata, M., Yoshimura, A., Mikura, J., Kawai, J., Kawai, J., Kawai, J., Kawai, J., Kawai, J., Adaki, J., Adaki, J., Adaki, J., Adaki, J., Adaki, J., Adaki, J., Hayatsu, N., Imctani, K., Ishii, Y., Itoh, M., Kagawai, J., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sohino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from Japonica rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ladachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fuyimura, T., Fukuda, S., Hanagaki, T., Hara, Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Horta, I., Ishibiki, J., Ishikawa, M., Itoh, M., Kagawa, I., Kanagwa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kiuchi, S., Kishikawa, Hirozane, T., Kishimoto, N., Kodagashi, M., Kodama, T., Kojima, K., Kojima, Y., Kodono, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nilkura, J., Nishi, K., Nomura, K., Narikawa, R., Ohnoda, E., Ohno, M., Ohtsuki, K., Sakai, C., Sakai, K., Sakai, E., Ohno, M., Sano, H., Satoh, K., Tagami, M., Tagami, M., Tagami, A., Suzuki, K., Satoh, K., Tagami, M., Tagami, R., Tawana, A., Suzuki, K., Satoh, K., Kie, Q., Yahagi, W., Tagama, T., Taunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, L., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : http://cdna01.dna.affrc.go.jp/cDNA/
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REFERENCE
AUTHORS
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JOURNAL
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COMMENT

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Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausberg, R.L., Zeeberg, B., Buetow, K.H., Schefer, C.R., Bhat, N.K.,
Altschul, S.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, R.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, R.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Ubdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Worley, K.C., Hale, S., Garcia, A.M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitning, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitning, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI 02-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (01-A02-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Baylor Human Genome Sequencing Center
CDNA Library Preparation: Baylor Human Genome Sequencing Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
                                                                         /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Mismatches:
Indels:
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BC101314
                                                                                                                                                                                                                                                                                       Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 ArgProLeuSerProProProAlaAla 41
                                                                                                     /mol_type="mRNA"
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Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC101314.1 GI:71680577
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1 (bases 1 to 3699)
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Best Local Similarity:
Query Match:
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                           PEATURES
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ROD 14-FEB-1996
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Homo sapiens HNF-3/forkhead-like protein 1 (HFH1) gene, complete
                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 3956)

Beru, N., McDonald, J. and Goldwasser, B.
Activation of the erythropoietin gene due to the proximity of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                 2766927
Original source text: Mus musculus (strain ICFW) (clone: 18C.)
adult spleen DNA.
Draft entry and computer-readable copy of sequence [1] kindly
                                                               MUSERPB 3956 bp DNA linear R
Mouse rearranged erythropoietin (epo) gene, 5' flank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/olone="18C."
/cell_line="erythroleukemic cell line IW32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3956
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Matches:
Conservative:
Mismatches:
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Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="spleen"
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complement(<1. .570)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(251. .383)
/note="Bl repeat element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                    submitted by N.Beru, 02-AUG-1989.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /bound_moiety="Sp1 3"
1496. 1501
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/note="ORF; putative"
                                                                                                                                                                                                                                                                                     expressed gene
DNA 8 (4), 253-259 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
1188. _1193
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AF225950.1 GI:12655883
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Center, Stanford University School of Medicine, Stanford, CA 94305 Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAM Plate: 7 Row: m Column: 7.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 02-FEB-2004
                                                                                                                                                                                                                                              /clone="IMAGE:40024855"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter, J.C., Adams, M., Li, P.W. and Myers, B.W.
Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 0171042-A 2348 27-SEP-2001;
PE Corporation (NY) (US)
Location/Qualifiers
1. .3840
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 TTGCCATCCTCTCTGGCCTTGTTGTCC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACCATCCGCCAGCGCCGCCGCCGGT 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                /mol_type="mRNA"
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AGGEGARSKPTRRPKPPYSYIALIMAIRDSAGGRITHERIBYIAGKPPPRFGSY
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RAVDPAGERBERAFGLIPARAPPRAPARAPRWRSPRAKDERSKAFARSSEFALDSI
LRKEPRSRLKDTAFGTTLOMGAPCPPLPARPALLEPAPCRALLPLAYGESPARL
GARBARVPPTAPPLLLAPLPAAAPAKPLRGPAAGGAHLVCPLRLPAALQAASVRRPGB
                                                                                                                                                      Dieller, A., Pasche, B. and Zoll, B.
Bieller, A., Pasche, B. and Zoll, B.
Bieller, A., Pasche, B. and Zoll, B.
Bieller, A., Pasche, B. and Zoll, B.
Submitted (17-JAN-2000) Institute of Human Genetics, University of Goettingen, Heinrich-Dueker-Weg 12, Goettingen 37073, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Jote="forkhead transcription factor; similar to Mus musculus HNP-3/forkhead homolog 1 like encoded by GenBank Accession Number AF010405 and Rattus norvegicus HNF-3/forkhead homolog-1 encoded by GenBank Accession Number L13201"
Hominidae; Homo.
1 (bases 1 to 4109)
Bieller,A., Pasche,B., Frank,S., Glaser,B., Kunz,J., Witt,K. and
                                                                     Zoll,B.
Isolation and Characterization of the Human Forkhead Gene FOXO1
DNA Cell Biol. 20 (9), 555-561 (2001)
11747606
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1737. .2948
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Minimum DB Maximum DB

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Database

Result No.

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Add$329 Novel hum
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Aby34143 Breast ca
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Adf$1022 Coln
Adf$1042 Plant cDN
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Ad437426 Human res
Ad437496 Human res
Ad437496 Human res
Ad197496 Human res
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-DB=N Geneseq -QFWT=fastap -SUFFIX=oligo_p2n.rng -MINMATCH=0.1 -LOOPCL=0
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The invention describes a new isolated polymucleotide (I) encoding a polypeptide with biological activity comprising: a nucleotide sequence of SEQ INOS: 1-567 (Fully defined); a nucleotide sequence that hybridizes to the sequence having greater than 99% sequence identity with the sequence of (i). Also described are: a(n) (expression) vector comprising (I); a host cell genetically engineered to comprise (I) operatively, associated with a regulatory sequence that modulates expression of the polymucleotide in the host cell; an isolated polypeptide comprising a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide (is: a polypeptide encoded by (I); or a polypeptide encoded by a sequence of SEQ ID NOS: 568-1134 (fully defined), where the polypeptide of (is: a polypeptide encoded by (I); or a polypeptide of (is) and a sequence of SEQ ID NOS: 1567; a composition comprising the polypeptide of (is) and a carrier; an antibody directed against the polypeptide of (is) and a carrier; an antibody directed against the polypeptide of (is) and a carrier; an antibody directed against the polypeptide of (is) and a carrier; an antibody directed against the polypeptide of (is) and a collypeptide of (is) and a collection of polymucleotides, where the collection comprising of at collection of polymucleotides, where the collection comprising of at collection of polymucleotides, where the collection comprising an of the sequences of SEQ ID NOS: 1-567. (I) is a polymucleotide of (is) and a collection of polymucleotides, where the collection comprising of a carrier; which comprises any of the amino acid sequence of SEQ ID NOS: 1-567. (I) is a polymucleotide with biological activity, which comprises any of the amino acid sequence of SEQ ID NOS: 1-567. (I) is a polymucleotide of (is) and activity, which are useful for treating a disease or disorders or other traits, in assessing biodiversity, and for producing many other composition and method are useful for treating a disease, birrah and product dependence of sequence or
DNA purification; protein purification; osteoarthritis; antiarthritic; osteopathic; musculoskeleral disease; osteoporosis; endocrine disease; periodontal disease; antiinflammatory; mouth disease; burns; injury; peripheral neuropathy; Alzheimers disease; neuroprotective; nootropic; degeneration; parkinsons disease; antiparkinsonian; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide encoding a polypeptide with biological activity, useful for treating a disease or disorder, e.g. osteoarthritis, burns, CNS and peripheral disease, stroke, autoimmune disorders, viral
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Goodrich R, Chen R;
                                                                                                                         cerebrovascular ischemia, cerebroprotective, vasotropic, cardiovascular disease, autoimmune disease; immunosuppressive; immune disorder; viral infection; virucide; infection; cancer;
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Xue A, Asundi V, Zhao Q, Wang D,
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Alignment Scores:

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The present invention describes human nucleic acid-associated proteins designated NAAP-1 to NAAP-57. The human NAAPs have cytostatic, antiarteriosclerotic, anti-HIV, antiallergic, cerebroprotective, antiparkinsonian, anticonvulsant, nootropic, neuroprotective, antinatentory, ophthalmological, thyromimetic, antiarthritic, hepatotropic, antibacterial, virucide, protozoacide, antiparasitic and implicate activities, and can be used in gene therapy. The NAAP protein and polymucleotide sequences can be used in gene therapy. The NAAP protein preventing diseases or conditions associated with the decreased expression or overexpression of NAAP, such as cell proliferative diseases (e.g. cancer, atherosclerosis, hepatitis), neurological disorders (Parkinson's disease, Alzheimer's disease, stroke, epilepsy), developmental disorders (renal tubular acidosis, anaemia, glaucoma,
New human nucleic acid-associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
                                                                                                                                                                                                                                                                                                                                                                human; nucleic acid-associated protein; NAAP; cytostatic; antiateriosclerotic; auti-HIV; antiallergic; cerebroprotective; antianteriosclerotic; auti-HIV; antiallergic; cerebroprotective; antiinflammatory; ophthalmological; thyromimetic; antiarthritic; hepatotropic; antibacterial; virucide; protozocacide; antiparastic; fungicide; gene therapy; cell proliferative disease; cancer; atherosclerosis; hepatitis; neurological disorder; Parkinson's disease; Alzheimer's disease; stroke; epilepsy; developmental disorder; renal tubular acidosis; anaemia; glaucoma; hypothyroidism; autoimmune disorder; inflammatory disorder; ADS; allergy; atopic dermatitis; arthritis; infection; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forsythe IJ, Gorvad AE, Griffin JA;
5, Lee EA, Lee SY, Li JX, Marquis JP;
7, Sprague WW, Swarnakar A, Tang YT;
                                                                                                                                                                                                                                                                                                                           Human nucleic acid-associated protein NAAP-41 cDNA SEQ ID NO:98
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                                                                                          704 CGAGCCGAGAAATTGATGTGCTCATCTTCAAGAAGC
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Elliott VS, Emerling BM, Forsythe IJ, (
Azalle AE, Khare R, Lal PG, Lee EA, Lee
Ramkumar J, Richardson TW, Sprague WW,
Chawla NK, Warren BA, Yue H;
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2002US-0347633P.
2002US-0351749P.
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P-PSDB; ADD01203.
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                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                comprising: a sequence encoding a sequence comprising 11-1518 amino acids is a sequence comprising 11-1518 amino acids is a sequence comprising 190-8144 bp; or a sequence that selectively hybridises to, or having at least 60$ identity with the 11-1518 amino acid or 190-8144 nt sequence. The polypeptide and the nucleic acid are useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer in a patient. The polymucleotides of the invention can be used to treat disorders by gene therapy. This polymucleotide represents a breast specific related sequence of the
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                                                                                                                                                       New isolated nucleic acid molecule, useful for treating breast cancer, and diagnosing or monitoring the presence of metastases of breast cancer
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                                                                                                                                                                                                                                                                                     invention relates to a novel isolated nucleic acid molecule
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                                                                   Recipon H,
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                        (DIAD-) DIADEXUS INC.
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hypothyroidism), autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis, arthritis) and infections (e.g. bacterial, viral, parasitic, protozoal, fungal). The present sequence encodes human NAAP-41, from the present invention.
                                                                                                                                                                                                                                                                                                                                   358 AGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGC
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                                                                                                                                                                                                                                                                           41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
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                                                        Sequence 2392 BP; 471 A; 743 C; 674 G; 504 T; 0 U; 0 Other;
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The invention discloses a polymuclectide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel colypeptides. Also claimed is a polypeptide encoded by the polymuclectide, immunologically assaying the polymeptide or peptide or tits partial peptide, immunologically assaying the polymeptide or peptide or tits partial peptide, immunologically assaying the polymeptide or peptide of the polymuclectide by contacting the polymeptide or peptide with the antibody of the encoded protein, and observing the binding between the two, a transformant carrying the polymuclectide in an expressible manner and an antisense polymuclectide. The oligonuclectide or sa useful as a primer for synthesising the polymuclectide, or as a probe for detecting the polymuclectides and encoded proteins are useful as pharmaceutical agents and many disease-related proteins are useful as pharmaceutical agents and adaptosetic marker or medicines for regulation of their expression and activity, or as targets of gene may be included in their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or call regeneration. Membrane proteins, signal transduction-related proteins, transcription-related proteins, disease-related proteins and genes cenceding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases, cancer, tumours. The cDNA may be used to regulate cenceding them can be used as indicators for diseases (e.g. osteoporosis, neurological diseases) on of the encoded protein to creat diseases. The esequence presented is a cDNA of the invention. Note: Some of the sequence cata for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office.
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Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or
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signal transduction-related protein; transcription-related protein; osteoporosis; neurological disease; cancer; tumour.
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                                                                                                                                                                                                                                                                                                                   "Clone KIDNE20157100 protein"
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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25-JAN-2002; 2002US-00350978.
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
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P-PSDB; ADB64615.
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Best Local Similari
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                                                 LeuArgThrProLeuArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCys
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                 GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
                                CAGAGAGCATTACCTTCATCTCGGCTCTGAGCCGGCCCTTGAGTCCCCCACCTGCT
                                                                                      AlaGlyIleAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
                                                                                                                                CTGAGGACTCCACTGAGGGGACTGCTGAAGCCAACTGGGGCCAAGGAGCACAATGGAGTGC
                                                                                                                                                        ProProAlaLeuIleValHisProProAlaGlyGlyMetAlaSerGly-SerSerGlnPr
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Reinhard C, Randazzo F, Kennedy GC, Pot D. Lamson G;
Crkenjakov R, Drmanac S, Dickson M, Labat I;
z D, Kita D, Garcia V, Jones LW, Strache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; gene therapy; colon cancer; prostate cancer; cancer; lung cancer; cancer detection; ss.
                                                                                                                                                                                                                                                                                                                                            TCGAGCCGAGAAATTGATGCTGCTCATCTTCAAGAAGC 828
                                                                                                                                                                                                                                                                                                                                   sArgAlaGluLysLeuMetCysSerSerSerArgSer 212
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 2132
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Drmanac R, Crkenjakov R
Leshkowitiz D, Kita D,
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02-JUL-1999;
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The present sequence is one of 1351 sequences in a library of human polymucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polymucleotides. The probes can be used for chromosome mapping of the polymucleotides and for detection of transcription levels. Ribozymes or antisense oligonucleotides can be generated. The polymucleotides and the products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polymucleotides and proventive interventions. The polymucleotides, polypeptides and preventive them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia, dysplasia and hyperplasia
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Or
                                                   Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences.
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WPI; 2001-091805/10.
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diseases of the lung; transgenic animal; gene;
                                         WO200268633-A2
  non-cancerous
                      Homo sapiens
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                                                                                                                                                                                                          The present invention provides human breast specific coding sequences and proteins. These can be used in the diagnosis and treatment of breast cancer and non-cancerous diseases of the breast. The present sequence is a coding sequence of the invention
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                                                                                                                                              New breast specific nucleic acids and proteins, useful for identifying, diagnosing, monitoring, staging, imaging, and treating breast cancer an non-cancerous disease states in breast tissue, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene therapy, vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer;
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Liu C;
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The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, they are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence encodes a lung specific nucleic acid
                                                                                                                                                                                                                                                                                           New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 266-267; 389pp; English
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21-NOV-2001; 2001WO-US043612.
                                                           22-NOV-2000; 2000US-0252500P.
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Best Local Similarity:
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2000US-0225268P.
2000US-0225270P.
2000US-0225447P.
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2000US-0189874P.
2000US-0190076P.
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2000US-0225267P
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25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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16-MAR-2000;
17-MAR-2000;
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14-JUL-2000;
26-JUL-2000;
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14-AUG-2000;
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07-JUN-2000;
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05-SEP-2000;
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                                        09-AUG-2001
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357 AGCCCCCAACCCGCCGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGC 416
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                                                                                                                                                                                                                                                                                                                          The invention describes an isolated human nucleic acid (I) encoding any of 120 10-1533 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This sequence
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                                                                                                                                                                                                                                         New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1977 BP; 393 A; 631 C; 554 G; 399 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                   Claim 1; Page 205-206; 389pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encodes a lung specific nucleic acid
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                                                                                               21-NOV-2001; 2001WO-US043612.
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Query Match:
                                        WO200268633-A2
             Homo sapiens.
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2000US-0249207P.
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2000US - 0249212P.
2000US - 0249214P.
2000US - 0249214P.
2000US - 0249215P.
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2000US-0249297P
                   29-58P-2000;
02-0CT-2000;
02-0CT-2000;
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02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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(HUMA-) HUMAN GENOME SCI INC

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cuplynucleotides may be used to produce the secreted (I), by inserting the
nucleic acids into a host cell and culturing the cell to express the
concern and cancer metastesses of haematopoietic-related diseases, especially
cancers and cancer metastesses of haematopoietic-derived cells. AAK64703
cancers and cancer metastesses of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention
                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                       Disclosure; SEQ ID NO 21882; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4583 BP; 1269 A; 1249 C; 1011 G; 1054 T; 0 U; 0 Other;
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Ruben SM;
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Barash SC,
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                                 WPI; 2001-483426/52.
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Best Local Similarity:
Query Match:
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Rosen CA,
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are associated with carcinomas. The sequences are useful for: (1) for screening drug candidates; (1i) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (1ii) for screening of a bioactive agent capable of modulating the activity of CAP; (1v) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                                                                                     present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002182586A1, for which no sequence data was published
                        Claim 1; SEQ ID NO 2002; Opp; English.
                                                                                     The
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Seguence 261817 BP; 71088 A; 59621 C; 57924 G; 73184 T; 0 U; 0 Other;

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se; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
         261817
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                                                                                                     241066 CTTCCATCCAGCCTCGCTCTCCTGAGCCGCCC 241098
         Length:
Matches:
Conservative:
Mismatches:
                                                                                            34
                                                                                            LeuProSerSerLeuAlaLeuLeuSerArgPro
                                                                          US-09-989-890-238 (1-212) x ACN45182 (1-261817)
                                               Indels:
                                                        Gaps:
                                                                                                                                                   ADQ63387 standard; cDNA; 1635 BP.
                                                                                                                                                                                                          Novel human cDNA sequence #548.
                                                                                                                                                                                                                                                                                                                                                  21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
                                                                                                                                                                                                                                                                                                                                21-JAN-2004; 2004EP-00001196.
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                                                                                                                                                                                        (first entry)
                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                          Homo sapiens.
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Alignment Scores:
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                                                                                            24
                                                                                                                                                                      ADQ63387;
                                            Query Match:
DB:
                                                                                                                                                                                                                                                         cancer.
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Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

Claim 1; SEQ ID NO 548; 2449pp; English.

ŝ Ishii

Sato H,

Wakamatsu A,

I T, Wahr

Sugiyama T, Otsuki T , Isono Y, Nagai K,

Yamamoto J,

Isogai T,

WPI; 2004-535376/52. P-PSDB; ADQ65575.

(REAS-) RES ASSOC BIOTECHNOLOGY

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The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morpid states. They are also useful for treating osteopropis, neurological diseases, Alzhaimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteopropis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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                                                                                                                                                                             Seguence 1635 BP; 334 A; 466 C; 505 G; 330 T; 0 U; 0 Other;
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Nagai K,
                                                                                                                                                                                                                                                                                                                                                   US-09-989-890-238 (1-212) x ADQ63387
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09-MAY-2003; 2003JP-00131392.
                                                                                                                                             sequence of the invention.
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Isono Y,
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P-PSDB; ADQ67127.
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Query Match:
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Yamamoto J,
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This invention relates to a novel method for modulating the expression of a target gene in a cell. Specifically, it refers to the introduction into a call of a polynucleotide that forms a duplex region with an mRNA transcribed from the target gene, where the duplex region with an mRNA transcribed from the target gene, where the duplex region comprises a mammalian miRNA at a post-transcriptional level. The present invention cell. differentiation of a mammalian cell, differentiation of a mammalian cell, differentiation of a mammalian cell in the post-transcriptional phase, which comprises mammalian cell in the post-transcriptional phase, which comprises introducing a plasmid vector comprising a promoter and nucleic acid molecule expressing an miRNA or siRNA silencing precursor to the miRNA. Accordingly, it provides a cell therapy method for treating cancer, immune disease, nerve disorder (e.g. amyotrophic lateral sclerosis, parkinson's disease, or Alzheimer's disease) or an inflammatory disease. By introducing into the cell the miRNA, siRNA silencing precursor to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating expression of a target gene in a cell, for treating cancer, an immune disease, or a nerve disorder, comprises introducing into the cell a polynucleotide that forms a duplex region with an mRNA transcribed from the target gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune disease; nerve disorder; amyotrophic lateral sclerosis;
Parkinson's disease; Alzheimer's disease; inflammatory disease;
siRNA silencing precursor; cytostatic; immunosuppressive; nootropic;
neuroprotective; antiinflammatory; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds; miRNA; microRNA; ontogenesis; cell therapy; cancer;
                                     Sequence 2816 BP; 522 A; 878 C; 818 G; 598 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human fork head domain protein DNA, target gene of miRNA.
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Mismatches:
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                                                                                                                                                                                                                                                                                          261 TCCTCACTGGCCCTTCTATCCAGGCCCCTT 232
                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                    SerSerLeuAlaLeuLeuSerArgProLeu 35
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                                                                                                                                                                                                                                                                                                                                                                                   ADR83528 standard; DNA; 3421 BP
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sequence of the invention.
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                                                                                                                                                       Similarity:
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                                                                           Alignment Scores:
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The invention relates to a novel method for in vitro detection of systemic inflammatory response syndrome (SIRS). The method comprises detecting abnormal expression of disease-related genes, or their associated peptides. The method of the invention demonstrates antibacterial, immunosuppressive and antiinflammatory applications and may be used for early differential diagnosis, monitoring progression, mortem diagnosis of systemic inflammatory response to treatment and for post mortem diagnosis of systemic inflammatory response syndrome, sepsis and sepsis-like conditions. The recombinant or synthetic nucleic acid sequences of the invention, or derived proteins or peptides, may be useful as calibrants in assays for the specified diseases, for evaluating activity or toxicity in screening for active agents and/or for preparation of agents for treatment or prevention of the specified diseases. The current sequence is that of a human SIRS/sepsis diagnostic
miRNA or the plasmid vector. As such, they can be developed into pharmaceutical compositions that exhibit cytostatic, immunosuppressive, nocropic, neuroprotective and antiinflammatory activities and hence can be used for immunocherapy. This polymucleotide sequence is a human target gene whose expression is modulated by miRNAs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vitro detection of systemic inflammatory response syndrome and related conditions, for e.g. monitoring progression, comprises detecting abnormal expression of disease-related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deigner H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Systemic inflammatory response syndrome; SIRS; antibacterial; immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.
                                                                                                            Sequence 3421 BP; 852 A; 859 C; 805 G; 905 T; 0 U; 0 Other;
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Conservative:
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                                                                                                                                                                    Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACF87489 standard; DNA; 5722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2003; 2003DE-01015031.
08-AUG-2003; 2003DB-01036511.
02-SEP-2003; 2003DE-01040395.
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Best Local Similarity:
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patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct_sequences. Purthermore, a number of arbitrary SEQ ID No.8 are disclosed within the specification, however, these have not been taken into account during indexing due to inconsistencies in application and
  DNA fragment of the invention. Note: The sequence data for this
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Sequence 5722 BP; 1454 A; 1366 C; 1290 G; 1612 T; 0 U; 0 Other;

Eormat

5722 10 0 0 0 Length: Matches: Conservative: Mismatches: 551 GCGGGCCTGCCCTCGGCCTGCCGCT 580 AlaGlyLeuProSerAlaSerAlaAlaAla 61 Indels: Gaps: US-09-989-890-238 (1-212) x ACF87489 (1-5722) 169 10.00 100.0% 100.0% 4.7% Best Local Similarity: Percent Similarity: Alignment Scores: 25 Query Match: ઠ 셤

ACF87572 standard; DNA; 5722 RESULT 15

(first entry) 02-JUN-2005 ACF87572;

ВР

Human SIRS/sepsis diagnostic marker DNA fragment 6432.

Systemic inflammatory response syndrome; SIRS; antibacterial; immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.

Homo sapiens.

WO2004087949-A2.

14-OCT-2004.

31-MAR-2004; 2004WO-EP003419.

2003DE-01015031 02-APR-2003;

08-AUG-2003; 2003DE-01036511. 02-SEP-2003; 2003DE-01040395.

(SIRS-) SIRS LAB GMBH.

Deigner Zipfel PF, Straube E, Saluz H, Russwurm S, Reinhart K, WPI; 2004-748070/73. In vitro detection of systemic inflammatory response syndrome and related conditions, for e.g. monitoring progression, comprises detecting abnormal expression of disease-related genes.

Disclosure; Page; 75pp; German.

The invention relates to a novel method for in vitro detection of systemic inflammatory response syndrome (SIRS). The method comprises detecting abnormal expression of disease-related genes, or their associated peptides. The method of the invention demonstrates antibacterial, immunosuppressive and antiinflammatory applications and may be used for early differential diagnosis, monitoring progression, assessing risk, assessing the likely response to treatment and for post mortem diagnosis of systemic inflammatory response syndrome, sepsis and sepsis-like conditions. The recombinant or synthetic nucleic acid sequences of the invention, or derived proteins or peptides, may be useful as calibrants in assays for the specified diseases, for evaluating activity or toxicity in screening for active agents and/or for

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The present invention describes a polynucleotide library (I) useful in the molecular characterisation of a carcinoma, comprising a pool of polynucleotides or its subsequences which are either underexpressed or overexpressed in tumour cells, and correspond to any of the polynucleotide sequences chosen from the 468 sequences given in ABV94010 to ABV94477. Also described: (1) a polynucleotide array (II) useful for the prognosis or diagnostic of tumour, comprising (I); and (2) detecting (MI) differentially expressed polynucleotide sequences which are correlated with a cancer, involves obtaining a polynucleotide sample from a patient, and reacting the polynucleotide sample obtained with a probe
preparation of agents for treatment or prevention of the specified diseases. The current sequence is that of a human SIRS/sepsis diagnostic marker DNA fragment of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published part_sequences. Purthermore, a number of arbitrary SEQ ID No.s are disclosed within the specification, however, these have not been taken into account during indexing due to inconsistencies in application and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotide library useful in molecular characterization of a carcinoma, comprising a pool of polynucleotide sequences or its subsequences which are either underexpressed or overexpressed in tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fert
                                                                                                                                                                                Sequence 5722 BP; 1454 A; 1366 C; 1290 G; 1612 T; 0 U; 0 Other;
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Best Local Similarity:
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BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;

Sequence 5723

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immobilised on a solid support, where the probe comprises any combination of the polymucleotide sequences of (1) or its expression products encoded by polymucleotide sequences of (1), and detecting the reaction product.

(I) have cytostatic activities and can be used as anti-tumour agence. (1) is useful in molecular characterisation of a carcinoma. (I) and (II) are useful for the prognosis or diagnostic of tumour, in differentiating a normal cell from a cancer cell, detecting a hormone sensitive tumour cell, differentiating a tumour with lymph nodes from a tumour without lymph nodes, differentiating antercycline-sensitive tumours, and classifying good and poor prognosis primary breast tumours, and classifying good and poor prognosis primary breast tumours. (1) is useful for large-scale molecular cancer treatment, and for detecting differentially expressed genes that correlated with a cancer
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Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;

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20000
                           Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                 52 AlaGlyLeuProSerAlaSerAlaAla 61
                                                                             US-09-989-890-238 (1-212) x ABV94143 (1-5723)
         169
10.00
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4.7%
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Best Local Similarity:
Alignment Scores:
                                                Query Match:
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ADN06031 standard; cDNA; 5723 (first entry) 01-JUL-2004 ADN06031; RESULT 17 g

ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis. Antipsoriatic cDNA sequence #1254.

Homo sapiens.

WO2004028479-A2.

25-SEP-2003; 2003WO-US030907. 08-APR-2004.

25-SEP-2002; 2002US-0414006P

(GETH) GENENTECH INC.

Schoenfeld J, Williams PM, Wood WI; Clark H, Jackman J, s, Bodary Ë

WPI; 2004-305105/28. P-PSDB; ADN06032.

New PRO nucleic acid or polypeptide, useful for preparing a pharmaceutical composition for diagnosing or treating psoriasis in a mammal.

Claim 1; SEQ ID NO 2426; 3069pp; English.

The invention relates to novel polynuclectide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polynuclectides of the invention.

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The invention relates to a compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding forkhead box 01A, where the compound is at least 70% complementary to a nucleic acid molecule encoding forkhead box 01A and modulates expression of forkhead box 01A by at least 10%. The compound is useful for treating an animal having a disease or condition associated with forkhead box 01A, e.g. a hyperproliferative disorder (cancer, preferably rhabdomyosarcoma), or type 2 diabetes. This sequence corresponds to the human foxhead box 01A to which the oligonucleotides of the invention are targeted.
                                                                                                                                                                                                                                                                                                                              88; cytostatic; antidiabetic; foxhead box O1A inhibitor; forkhead box O1A; hyperproliferative disorder; cancer; rhabdomyosarcoma; diabetes; H-ras gene; antisense; gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           targeted to
for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shutter JR;
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Matches:
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Indels:
                                                                                                                                                    551 GCGGGCCTGCCCTCGGCCTCGGCTGCCGCT 580
                                                                                                                                     52 AlaGlyLeuProSerAlaSerAlaAlaAla 61
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                                                                                                           US-09-989-890-238 (1-212) x ADN06031 (1-5723)
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                                                                                   Gaps:
                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                     Human foxhead box 01A sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2003; 2003WO-US030352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2002; 2002US-00260203.
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(ISIS-) ISIS PHARM INC
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Best Local Similarity:
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                                        Percent Similarity:
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Alignment Scores:
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Pred. No.:
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                                                                                                                                                                                                                                                ADN97714;
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DB:
              Pred. No.:
                                                                                                                                                                                           RESULT 18
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ACN39628;
                                                     Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                      RESULT 20
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                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; forkhead box O1A; gene; da; antisense oligonucleotide;
hosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
5-methylcytosine; hyperproliferative disorder; cancer; rhabdomyosarcoma;
type 2 diabetes; cytostatic; antidiabetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a compound targeted to a nucleic acid molecule encoding the human forkhead box OlA polypeptide. The compound is an antisense oligonucleotide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothicate linkage, at least one modified sugar moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least une doiling nucleobase comprising a 5-methylcytosine. The antisense compounds are useful for modulating the expression of the human forkhead box OlA polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer, preferably rhabdomyosarcoma, and type 2 diabetes. This sequence represents DNA encoding the human forkhead OlA polypeptide of the invention.
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                                                                                      AlaGlyLeuProSerAlaSerAlaAlaAla 61
US-09-989-890-238 (1-212) x ADN97714 (1-5723)
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386. .2353
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VENIANT-ELLISON M.
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(LIND/) LINDBERG R A.
(SHUT/) SHUTTER J R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dobie KW, Bhanot S,
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P-PSDB; ADN40823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004097459-A1.
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Length: Matches:

169 10.00

Alignment Scores: Pred. No.:

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the intention retains to numean tumour-associated antigenic target (1747) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide acquences at least 80% identical to the TAT nucleic acids and polypeptides, expression vectors and host cells comprising a TAT nucleic acids and polypeptides; an antibody specific for a TAT polypeptide; peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; an antibodis and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancer, pancreatic cancer, cervical cancer, colorects of the central cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention
                                                                                                                                                                                                                                                                                                                                                                                                       Tumour-associated antigenic target (TAT) cDNA DNA270254, SEQ ID NO:3896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour-associated antigenic target, TAT; human; overexpression; ctumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; certical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping; gene therapy; cytostatic; gene; ss.
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  Conservative:
Mismatches:
                                                                                                                                                                       551 GCGGGCCTGCCCTCGGCCTGCCGCT 580
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                                           Indels:
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                                                                                                       (1-5723)
                                                                                                                                                   52 AlaGlyLeuProSerAlaSerAlaAlaAla
                                                                    Gaps:
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                                                                                                         US-09-989-890-238 (1-212) x ADN40650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABM81512
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us-09-989-890-238.oligo_p2n.rng

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The present invention relates to a method (M1) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 2147; 2938pp; English.
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US-09-989-890-238 (1-212) x ADF81591 (1-5769)
                                                                                                                                                                                                                                      Cytostatic; Gene therapy; leukaemia; ss.
                                                                                                                                                                                                     Leukaemia-related DNA sequence #2147.
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UNIV LUDWIG MAXIMILIANS.
HAPERLACH T.
SCHOCH C.
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Eils R, Brors B, Mergenthaler S;
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                                                                                                   ВР
                                                                                                   ADF81591 standard; DNA; 5769
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(SCHO/) SCHOCH (
(KERN/) KERN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient sample.
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                                                                                                                                                                                                                                                                       Unidentified.
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                                                                                                                                    ADF81591;
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                                                                  RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide. The polypeptide, agonist or an antagonist, antibody composition, and method are useful for diagnosing and treating an related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0 U; 0 Other;
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Sequence 5723 BP; 1454 A; 1366 C; 1291 G; 1612 T; 0
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiallergic; ds; gene; diagnosis.
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Query Match:
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Best Local Similarity:
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                                 Alignment Scores:
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ADY14881;

RESULT 21

8 셤 Dugas M;

Schnittger S,

5769 10 0 0 0

Query Match: DB:

Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.

30-MAR-2001; 2001WO-US008631 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

WO200175067-A2.

11-OCT-2001.

Homo sapiens.

DNA encoding novel human diagnostic protein #10524

(first entry)

13-FEB-2002

AAS74720;

AAS74720 standard; cDNA; 239 BP.

AAS74720/c

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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, ollogmers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                      Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder; ss.
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                                                                                                                                                                           DNA encoding novel human diagnostic protein #20857.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631.
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23-AUG-2000; 2000US-00649167.
                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                     13-FEB-2002
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AAS85053;
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73.

P-PSDB; ABG10533

(HYSE-) HYSEQ INC.

Claim 1; SEQ ID NO 10524; 103pp; English.

biodiversity.

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caction (PCR) primers, oligomers, and for chromesome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of (II) sequence (II) sequence tags for identifying expressed consists of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cuseful for generating antibodies against it, detecting or quantitating a cupypelement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forgentic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this conding sequence of the invention. Note: The sequence data for this conding sequence of the invention. Note: The sequence data for this conding sequence of the printed specification, but was obtained in all activity.
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Matches:
Conservative:
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5833 10 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

10.00 100.0% 100.0% 4.7%

Similarity:

Query Match: Local

Percent Similarity:

Score: Best

Alignment Scores: Pred. No.:

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RESULT 24

US-09-989-890-238 (1-212) x AAS85053 (1-5833)

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The present invention relates to the isolation of novel human polymentides exquences and their encoding polymentides. The novel polymentides exquences and their encoding polymentides. The novel polymentides exhibit activities relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, and stem cell growth factor activities. The polymentides are involved in the confideration, differentiation and survival of pluripotent and totipotent stem cells, and are useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and totipotent tissues. The polyment of bio-sensors. The polymential cells that can be used to augment or replace cells damaged by illness, autoimmune disease, used to augment or replace cells and regeneration of nerve and brain tissue and are useful for the treatment of central and peripheral nervous system diseases and neuropathelies, such as Alzheimer's parkhinson's disease, Huntington's disease, amyotrophic lateral sclerosis (ALS). The polymeptides are also involved in chemotactic or chemokinetic activity,
                                                                                                                                                                                                                                                                                 cell differentiation; totipotent; stem cell; transplantation; bio-sensor; neuroepithelial cell; autoimmune disease; neural cell; genetic disorder; nerve; brain tissue; central nervous system disease;
                                                                                                                                                                                                                                                                                                                                               peripheral nervous system disease; neuropathy; haematopoiesis; bone; myeloid disorder; lymphoid cell disorder; platelet disorder; tendon; regeneration; cartilage, tendon; ligament; nerve tissue growth; tissue repair; wound healing; burn; ulcer; osteoporosis; cancer; osteoporosis; cancer; osteoporosis; cancer; osteoporosis; cancer; osteoporosis; cancer; osteoporosis; cancer; immune deficiency; infection; autorimmune disorder; allergic reaction; thrombolysis; thrombosis; liver fibrosis; reperfusion injury; thrombolysis; thrombosis; cagulation disorder; hereditary disorder; biorhythm; circadian cycle; fertility; metabolism; catabolism; anabolism; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; haemostatic; vulnerary; antiulcer; osteopathic; antianthitic; varucide; antitheumatic; antidiabetic; antiasthmatic; cytostatic; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides for diagnosis, treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
                                                                                                                                                                                                                                                               angiogenesis; cytokine; cell proliferation; pluripotent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 691; 300pp; English.
131 CTTCCTTCAGCGTCAGCAGCTGGA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag; EST; ss
                                                                                ACD05845 standard; cDNA; 239
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                                                                                                                                                                            06-AUG-2003 (first entry)
                                                                                                                                                                                                                     Novel human contig #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-313249/30.
P-PSDB; ABO00768.
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                                                                                                                                ACD05845;
                                                                                                                                                                                                                                                                 Human;
                                             RESULT 25
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regulation of haematopoiesis and are useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia and cor for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, and periodontal disease. The polypeptides are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders infections, autoimmuned disorders (e.g. multiple sclerosis, reperfusion infections, autoimmuned disorders (e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis), allergic reactions and conditions, such as asthma or other respiratory problems. The polypeptides are involved in thrombolysis or thrombosis and are useful in treatment of various coagulation disorders (including hereditary disorders such as haemophilia) or to enhance coagulation and other causes. The polypeptides exhibit immune stimulating or immune concerns in treating wounds resulting from treatme diseases or cancer. They also inhibit the growth, infection or function of infectious generic such as bacteria, fungi, viruses, effect blorhythms or circadian cycles of rhythms, fertility of male or female subjects, metabolism, catabolism, and anabolism. Achosest effect blorhythms or circadian cycles of rhythms, fertility of male or female subjects, metabolism, as seeds. Note:

The sequence data for this patent did not form part of the printed cycles of this patent did not form part of the printed presents in electronic format directly from WIPO
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genome mapping; biodiversity; genetic disorder.
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Matches:
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STACHE-CRAIN B.
DICKSON M C.
JONES L W.
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(DICK/)
(JONE/)
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisenses bus or the purified polypeptide is useful for generating antisense of the purified polypeptide is useful for generating antisead sequences. Note: The present sequence for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; treatment; prevention; protein therapy; AIDS; gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; lymphoma; renal disease; inflammation; allergy; Alzheimer's disease; schizophrenia; cognitive disorder; prostate disease; skehetal; cardiac; muscle disorder; prostate disease; schebtal; cardiac; muscle disorder; pulmonary disorder; transplant rejection; osteoclast; osteoporosis; arthritis; malignancy; digestive; endocrine; infection; ss.
                                                                       polynucleotide sequences obtained from various cDNA libraries, useful
                                                                                          as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 496 BP; 108 A; 157 C; 121 G; 108 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 3937; 44pp; English.
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AAX37513 standard; cDNA; 546 BP.
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WPI; 2003-615964/58
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Best Local Similarity:
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02-OCT-1997;
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Query Match:
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This invention describes novel isolated human genes and the secreted proteins they encode. The products of the invention are useful for proteins they encode. The products of the invention are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polymucleotides.

C Specific uses are described for each of the 101 polymucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, contendegenerative disorders, developmental abnormalities and fetal contendegenerative disorders, letkemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, Albeimer's and cognitive disorders, pulmonary disorders, clasease, skeletal or cardiac muscle disorders, pulmonary disorders, cramsplant rejection, disorders involving ostecolasts such as costeoporosis, arthritis or malignancies, digestive/endocrine disorders, infections and AIDS: The human secreted proteins of the invention are represented in AAX37451-X37552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Central nervous system, CNS; autoimmune disease, rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
                                                                                                                                                                                                                                                                                                                                   New isolated human genes and the secreted polypeptides they encode.
                                                                                                                                                                                                          Young P;
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Carter KC, Endress GA,
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[, Yu G, Janat F, Ni J,
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                                             97US-0060843P.
97US-0060862P.
97US-0060866P.
97US-0060874P.
97US-0060880P.
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08-NOV-2000;
       acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
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2000US-0190076P

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2000US-021488P

2000US-021647P

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2000US-0232401P.
2000US-0233063P.
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23-AUG-2000;
30-AUG-2000;
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04-FEB-2000;
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2000US-0240960P. 2000US-0241221P. 2000US-0241785P. 2000US-0241786P. 2000US-0241786P.

2000US-0241808P

2000US-0237038P.

2000US-0237040P 2000US-0239935P 2000US-0241809P 2000US-024617P 2000US-0246474P 2000US-0246476P 2000US-0246477P 2000US-0246477P 2000US-0246478P 2000US-0246478P 2000US-0246524P 2000US-0246525P 2000US-0246525P 2000US-0246525P

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2000US-0246528P

2000US - 0249216P 2000US - 0249217P 2000US - 024924P 2000US - 0249248P 2000US - 0249245P 2000US - 0249264P 2000US - 0249265P

2000US-0249213P. 2000US-0249214P. 2000US-0249215P.

2000US-0249299P. 2000US-0249300P. 2000US-0250160P. 2000US-0250391P.

2000US-0251868P

2000US - 023499B P 2000US - 02354B4 P 2000US - 02358B4 P 2000US - 02358B5 P 2000US - 0236B5 P 2000US - 0236B9 P 2000US - 0236BP P 2000US -

2000US-0234223P. 2000US-0234274P. 2000US-0234997P.

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Alzheimer's disease, infection, ocular disorder, corneal infection, wound healing, epithelial cell proliferation, food additive.
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2000US-0225267P.
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2000US-0225757P
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21-SEP-2000;
21-SEP-2000;
                                                            Homo sapiens
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17-MAR-2000;
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19-MAY-2000;
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    The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (II), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include cautoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and anglogenesis, nervous system disorders e.g. Alzheimer's disease and amplotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. corneal infection, gastrointesinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. corneal infection, gastrointesinal disorders e.g. dysphagia, cancers and disorders e.g. malignancies, and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. respiratory disorders e.g. nonallergic chinitis, renal disorders e.g. cette kidney failure and blood related disorders e.g. myocardial cinfarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The colypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal tissue antigen; ss; antiinflammatory; neuroprotective;
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cardiovascular; autoimmune disease; rheumatoid arthritis;
hyperproliferative disorder; breast neoplasm; cancer;
cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cerebral ischaemia; angiogenesis; nervous system disorder;
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                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 478; 837pp; English
                                                                                                                                                          Ruben SM
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251999P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0259679P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                          Rosen CA, Barash SC,
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P-PSDB; AAU87558.
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Query Match:
                                                                                                                                                                                                                                                                                                  preservatives.
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Pred. No.:
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20000S-0241785P.
2000US-0241785P.
2000US-0241787P.
2000US-0241808P.
2000US-0241809P.
2000US-0241826P.
2000US-024647P.
2000US-0246475P.
2000US-0246476P.
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2000US-0246523P.
2000US-0246524P.
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2000US - 0249300P.
2000US - 0250L60P.
2000US - 0250391P.
2000US - 025198P.
                                                                                      2000US-0237038P.
2000US-0237039P.
2000US-0237040P.
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2000US-0249218P.
2000US-0249244P.
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2000US-0249264P.
2000US-0249265P.
2000US-0249297P.
                                                                2000US-0236370P.
2000US-0236802P.
2000US-0237037P.
                                   2000US-0236327P.
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2000US-0236369P.
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                             :000US-0235836P
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2000US-0249
2000US-0249
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                        29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
                                                                                                    02-0CT-2000;
13-0CT-2000;
20-0CT-2000;
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08-NOV-2000;
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17-NOV-2000;
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08-NOV-2000;
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The invention relates to novel mucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or amellorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (EIISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. Conservation, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial corders before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease consore as a food additive or preservative to increase or decrease consore examples of diseases and disorders treated by the nucleic acids and corders are given in the specification. The present sequence encodes a content of the invention. One sequence data for this patent content of the present sequence data for this patent content in the specification, but was obtained in
                                                                                                                                                                                                     New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and respiratory systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 da; gene; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; gene therapy; channel/transporter protein; rheumatoid arthritis; neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia; angiogenesis, nervous system disorder; Alzheimer's disease; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin aging; sumburn; transplantation;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 635; 642pp; English.
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                                                                                          Ruben SM;
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05-JAN-2001; 2001US-0259678P.
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                                          (HUMA-) HUMAN GENOME SCI INC.
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9.00
100.0%
100.0%
                                                                                          Rosen CA, Barash SC,
                                                                                                                                   WPI; 2001-488782/53.
P-PSDB; AAU21291.
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Best Local Similarity:
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2000US - 023499BP

2000US - 0235434P

2000US - 0235334P

2000US - 023634P

2000US - 023636P

2000US - 023703P

2000US - 02410P

2000US - 024178P

2000US - 0246477P

2000US - 0246477P
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2000US-0249613P
2000US-0249203P
2000US-0249209P
2000US-0249210P
2000US-0249211P
2000US-0249211P
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2000US-025198BP.
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2000US-0251990P.
2000US-0254097P.
2001US-0259678P.
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2000US-0249245P.
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05-DBC-2000;
06-DBC-2000;
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08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
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08-DBC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
25-SBP-2000)
27-SBP-2000)
27-SBP-2000)
29-SBP-2000)
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20-CCT-2000)
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
   2000US - 0179065P

2000US - 0186628P

2000US - 0186350P

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2000US - 021513F

2000US - 021647P

2000US - 0217487P

2000US - 022524P

2000US - 022527P

2000US - 022578P

2000US - 0229344P

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2000US-0231242P.
2000US-0231244P.
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2000US-0231414P.
2000US-0232080P.
2000US-023239P.
2000US-023239P.
2000US-023239P.
2000US-023239P.
2000US-023239P.
2000US-023239P.
2000US-023236P.
2000US-023236P.
2000US-023236P.
2000US-023240P.
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2000US-023240P.
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 chemotaxis; food additive
                                                                     WO200154472-A2
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14-Aug-2000;
14-Aug-2000;
14-Aug-2000;
14-Aug-2000;
14-Aug-2000;
14-Aug-2000;
18-Aug-2000;
22-Aug-2000;
22-Aug-2000;
22-Aug-2000;
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14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
                                   Homo sapiens
                                                                                                       02-AUG-2001
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14-SEP-2000;
 The invention relates to an isolated nucleic acid molecule encoding a channel/transporter protein or sequences at least 954 identical to a these. The nucleic acids and proteins encoded by them are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used to displancing a pathological condition or susceptibility to a complete of a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic in alleviating symptoms associated with the disorders and in diagnostic (BLISA). Disorders which are diagnosed or treated immunosorbent assays (BLISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. carchiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, carcest, cerebrovascular disorders e.g. cerebral infections caused by actreat or lives, and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxie. The polypeptides can also be used additive or preservative to increase or decrease conservative conservative to the center of primary conservative conservative to increase or decrease conservative con
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                                                                                                                                      Isolated nucleic acid molecule encoding a channel/transporter protein is used in preventing, treating or ameliorating a medical condition.
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                        Claim 1; SEQ ID NO 473; 809pp; English
                                                    Ruben SM;
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                  (HUMA-) HUMAN GENOME SCI INC.
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9.00
100.0%
100.0%
4.2%
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                                                  Rosen CA, Barash SC,
                                                                                     2001-476159/51.
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Best Local Similarity:
Query Match:
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inflammatory disorder; ischaemia-reperfusion injury; inflammatory beat disease; Crohn's disease; infectious disease; HIV infection; hepatitis infection; bacterial infection; fungal infection; parasitic infection; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; reproductive disorder; atheroselerosis; arrhythmia; myocarditis; renal disorder; acute glomerulonephritis; pyelonephritis; renal lithiasis; puoliferative disorder; cancerous diseases; human; gene;
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2000US-0220964P.
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2000US-0189874P
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2000US-0225757P.
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                                                                                                                                                                                                                           Homo sapiens.
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18-APR-2000;
19-MAY-2000;
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27-SEP-2000;
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02-OCT-2000;
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08-NOV-2000;

08-NOV-2000;
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17-NOV-2000;
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The invention describes an isolated polypeptide comprising an amino acid sequence at least 90% identical to: a polypeptide fragment, domain, epitope, or full-length protein of any one of 607 amino acid sequences (I) described in the specification; a polypeptide fragment of (I), or the encoded sequence contained in (II), having biological activity; or a variant, allelic variant, or a species homologue of (I). The polypeptides and nucleic acid molecules are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,
                                                                                                                                                                                                                                                        New polypeptides and nucleic acid molecules, useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions e.g. neural disorders, reproductive disorders or infectious
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                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 478; 413pp; English
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           2000US-0251856P.

2000US-0251868P.

2000US-0251869P.

2000US-0251980P.

2000US-0251990P.

2000US-0254037P.
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2000US-0251479P
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4.2%
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                                                                                                                                                                                                                 WPI; 2004-122079/12.
                                                                                                                            ROSEN C A.
RUBEN S M.
                                                                                                                                                        BARASH S C
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Best Local Similarity:
Query Match:
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           08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
08-DEC-2000; 2
11-DEC-2000; 2
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06-DEC-2000;
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(RUBE/) 1
(BARA/) 1
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18-MAY-2001; 2001WO-US016450

WO200190304-A2

29-NOV-2001

Homo sapiens.

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Percent Similarity:
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04-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins antissues disclosed in the specification. The nucleic acids, proteins antissues disclosed in the specification. The diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, lurg, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycocardial ischaemias; (d) wound healing infections diseases e.g. cerebral anoxia and epilepsy; and (f) infections diseases e.g. viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; BST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                            Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                           Claim 4; SEQ ID NO 488; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 562 BP; 126 A; 146 C; 134 G; 149 T; 0 U; 7 Other;
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             19-MAY-2000; 2000US-0205515P
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                                     (HUMA-) HUMAN GENOME SCI
                                                              Birse CE, Rosen CA;
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proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel
                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention provides the protein and coding sequences of
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Werhman T;
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A, Zhang J, Werhr
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2001US-0325448P.
2002US-0370620P.
25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SBP-2000; 2000US-00663870.
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ID ADJ43042 standard; cDNA; 717
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plant nutrition; apical dominance; dwarfism; early flowering; antiviral;

US2004016025-A1

antifungal.

Eukaryota.

22-JAN-2004

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The invention relates to plant nucleotide sequences that direct seed, leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid cor constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they sorghum, rice or wheat. The polynucleotides and the polypeptides they sorghum, rice or wheat. The polynucleotides and the polypeptides they sorghum, rice or wheat. The polynucleotides and the polypeptides they sorghum, rice or waster to masteriate to a manipulating crop plants to an improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants incur stress tolerance (e.g. salt, cold or drought) to ensure the plants early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence dare for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at segdata.uspto.gov/seguence.html.
                                                                                                                                                                                                                                                                                                                                                                                                New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance
                                                                                                                                                                                                                                                                                  T, Briggs SP, Cooper B, Glazebrook J;
Kreps J, Provart N, Ricke D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 717 BP; 181 A; 161 C; 198 G; 177 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; SEQ ID NO 4042; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          high nutritional value.
                                                                                                                                                                                                                                                                                    Moughamer
                                                                                                                                                                                                                                                                                                             Goff SA, Katagiri F,
                                            BRIGGS S P.
COOPER B.
GLAZEBROOK J.
                                                                                                                GOFF S A.
KATAGIRI F.
KREPS J.
PROVART N.
RICKE D.
BUDWORTH P. MOUGHAMER T.
                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-190374/18.
                                                                                                                                                                                     (PROV/) PROVAR
(RICK/) RICKE |
(ZHUT/) ZHU T.
                                                                                                                                                                                                                                                                                    Budworth P,
  (BUDW/)
                        (MOUG/)
                                                                                                                                           KATA/)
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                                                                                                                        GOFF/
                                                                                             GLAZ/)
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717 9 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 196 9.00 100.0% 100.0% 4.2% Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Local

US-09-989-890-238 (1-212) x ADJ43042 (1-717)

24 LeuProSerSerLeuAlaLeuLeuSer 32 366 ò

ADJ43040 standard; cDNA; 737 BP 06-MAY-2004 (first entry) ADJ43040;

Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolarance, salt tolerance; cold tolerance; drought tolerance; Plant cDNA #4040.

creccricircerrescectariance 401 LeuProSerSerLeuAlaLeuLeuSer 32

(1-737)

US-09-989-890-238 (1-212) x ADJ43040

24 427

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Life and/or stem. Definition of an operatively linked nucleic security.

Leaf- and/or stem. panicle. root- or pollen-specific or -preferential

or constitutive transcription of an operatively linked nucleic acid

segment. The invention also relates to a method for augmenting a plant

considered in the seed, leaf, stem, panicle, pollen, root or is constitutive

altered in the seed, leaf, stem, panicle, pollen, root or is constitutive

calcard, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,

corpum, rice or wheat. The polymucleotides and the polypeptides they

corpum, rice or wheat. The polymucleotides and the polypeptides they

corpus are useful for manipulating crop plants to alter or improve

phenotypic characteristies, to produce large quantities of oil or

proteins, to incur resistance to insecticides, viruses or fungi, and to

concern to incur resistance to insecticides, viruses or fungi, and to

concern to incur resistance to insecticides, rices or fungi, and to

concern to incur resistance to insecticides, rices or fungi, and to

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to plant nucleotide sequences that direct seed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glazebrook J;
e D. Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 737 BP; 192 A; 162 C; 213 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T, Briggs SP, Cooper B, Glaz
Kreps J, Provart N, Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   737
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                       26-SEP-2001; 2001US-0325448P
04-APR-2002; 2002US-0370620P
                                                                                                                                                                                            26-SEP-2002; 2002US-00260238
                                                                                                                                                                                                                                       26-SEP-2001; 2001US-0325277P
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9.00
100.0%
100.0%
4.2%
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Katagiri F,
                                                                                                                                                                                                                                                                                                                      BUDWORTH P.
MOUGHAMER T.
BRIGGS S.
COOPER B.
GLAZEBROOK J.
GOPF S. A.
KATAGIRI F.
KREPS J.
PROVART N.
RICKE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-190374/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SA,
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(RICK/)
(ZHUT/)
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DB:
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(GLAZ/)
                                                                                                                                                                                                                                                                                                                                               (MOUG/)
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U; 0 Other;

Sequence 792 BP; 193 A; 201 C; 142 G; 256 T; 0

792 0 0 0 0

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AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthric; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiant; cardiant; cardiant; cardiant; antianaemic; antiagoregant; haemostatic; vulnerary; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; cardiactan; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic; cording them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polymucleotides are useful for screening for sponists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections autoimmunity, genetic diseases, haematopoietic disorders, cancer, multiple sclerosis, depression, hinitis asthma, diabetes, cancer, multiple sclerosis, depression, hinitis, asthma, diabetes, cancer, multiple sclerosis, depression, hinitis, asthma disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
                                                                                                                                                    Human protein encoding cDNA sequence SEQ ID NO:280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 421; 1217pp; English.
                                  AAH99445 standard; cDNA; 792 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2000; 2000WO-US035017
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                              16-OCT-2001
                                                                        AAH99445;
RESULT 36
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soybean, alfalfa, sunflower; canola, cotton; peanut; tobacco; sugar beet, maize; barley; soorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to plant nucleotide sequences that direct seed-, leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant; gene; ss; transcription; plant genome augmentation; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moughamer T, Briggs SP, Cooper B, Glazebrook agiri F, Kreps J, Provart N, Ricke D, Zhu T;
               Length:
Matches:
Conservative:
Mismatches:
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                                                                                      Indels:
                                                                                                     Gaps:
                                                                                                                                                                             24 LeuProSerSerLeuAlaLeuLeuSer 32
                                                                                                                                           US-09-989-890-238 (1-212) x AAH99445 (1-792)
                                                                                                                                                                                                26-SBP-2001; 2001US-0325277P.
26-SBP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
                                                                                                                                                                                                                                                                                      ADJ43041 standard; cDNA; 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2002; 2002US-00260238.
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             215
9.00
100.0%
100.0%
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GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUDWORTH P. MOUGHAMER T. BRIGGS S P. COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-190374/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KREPS J.
PROVART N.
RICKE D.
                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                Plant cDNA #4041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004016025-A1
                                                Percent Similarity:
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota.
                                                                                                                                                                                                                                                                                                                          ADJ43041;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KREP/)
(PROV/)
(RICK/)
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(BRIG/)
(COOP/)
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(GOFF/)
                                                                                    Query Match:
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9
                                                                       Local
                                                                                                                                                                                                                                                                         ADJ43041,
                                                                                                                                                                                                                                                    RESULT
                                                                       Best
                                                                                                                                                                                                                                                                                          Human, cancer; ulcer; HIV infection; human immunodeficiency virus;

antinflammatory; antirheumatic; antiarthritic; immunosuppressive;

antiacterial; endocrine; cardiant; central nervous system; virucide;

anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

anti-Gogical; antiallergic; antiathmatic; antianaemic; casema;

dermatchogical; antiallergic; antiathmatic; antialabetic; cytostatic;

dermatchogical; antiallergic; antiatese therapy; vaccine; inflammation;

immunostimulant; gene therapy; antibense therapy; vaccine; inflammation;

antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;

cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

wenter disease; haematopoietic disorder; platelet disorder; asthma;

thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;

neurological disorder; ss.
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genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polymuclectides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html. \$

Sequence 824 BP; 209 A; 183 C; 236 G; 196 T; 0 U; 0 Other;

824 0 0 0 0 0 Length:
Matches:
Conservative:
Mismatches: Indel8: Gaps: US-09-989-890-238 (1-212) x ADJ43041 (1-824) 223 9.00 100.0% 100.0% 4.2% Percent Similarity: Best Local Similarity: ignment Scores: Query Match: No.

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ADZ14553 standard; DNA; 1119 BP RESULT 38 ADZ14553

ADZ14553;

(first entry) 16-JUN-2005 DNA (LOC221103) encoding a human tumor associated antigen Seq 69

ф. chromosome 11; tumor-associated antigen; antisense therapy; RNA interference; diagnosis; cytostatic; cancer; metastasis; gene;

Homo sapiens

WO2005030250-A2

07-APR-2005

23-SEP-2004; 2004WO-EP010697.

26-SEP-2003; 2003DE-01044799

(GANY-) GANYMED PHARM AG.

Tuereci O, Sahin U, Helftenbein G, Schlueter V;

WPI; 2005-285105/29. P-PSDB; ADZ14554.

Compositions for treating and diagnosing cancer, contain agents that inhibit activity or expression of specific tumor-associated antigens, or bind to these antigens or nucleic acid encoding them. Claim 1; SEQ ID NO 69; 388pp; German.

This invention relates to a novel pharmaceutical composition which comprises an agent that inhibits the activity or expression of a specific tumor-associated antigen (TAg). Specifically, it relates to tumor-associated antigens that are encoded by one of the following 75 nucleic acida sequences, fragments or derivatives thereof as given in the specification. The present invention describes antisense nucleic acids

that hybridize to these TAg polynucleotides that may be used for antisense therapy and RNA interference, as well as methods for diagnosing a disease associated with (abnormal) expression of TAG. Accordingly, it further relates to methods for determining regression, progression and onset of a disease by administering an antibody, optionally linked to a therapeutic or diagnostic agent, that binds to TAG. As such, cytostatic compositions derived thereof are used for treating a wide range of cancers and their metastases, where the agents that bind specifically to TAG, and the nucleir acids that encode them, are useful for diagnosis and monitoring. This polynucleotide is a human DNA sequence encoding a tumor associated antigenic protein of the invention. New genes that are up- or down-regulated in colorectal cancer, useful for diagnosing colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating colorectal cancer. Colorectal cancer; metastasis; differential expression; cytostatic; diagnosis; gene therapy; vaccine; gene; ss. 1. 1209 /*tag= a /product= "Metastatic colon cancer polypeptide" Sequence 1119 BP; 318 A; 273 C; 209 G; 319 T; 0 U; 0 Other; 1119 9 0 0 0 0 Gene up-regulated in metastatic colorectal cancer. Length: Matches: Conservative: Mismatches: Indels: Gaps: 801 TrgccArccrcrcrcGccrrGrrGrcc 827 US-09-989-890-238 (1-212) x ADZ14553 (1-1119) 24 LeuProSerSerLeuAlaLeuLeuSer 32 Location/Qualifiers (EOSB-) EOS BIOTECHNOLOGY INC. (UYCA-) UNIV CASE WESTERN RESERVE. Claim 5; Page 252; 260pp; English ВЪ ABQ81557 standard; cDNA; 1209 27-FEB-2001; 2001US-0272206P. 02-APR-2001; 2001US-0281149P. 17-APR-2001; 2001US-0284555P. 27-FEB-2002; 2002WO-US006001 (first entry) 296 9.00 100.0% 4.2% Mack DH, Markowitz SD; WPI; 2002-698677/75. Best Local Similarity: P-PSDB; ABP54691. WO200268677-A2 Percent Similarity: Homo sapiens. Alignment Scores: 30-DEC-2002 06-SEP-2002 ABQ81557; Query Match: . No. : ABQ81557/c RESULT 39 Score: à 셤

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The present sequence is the nucleotide sequence of a human gene that exhibits increased expression in metastatic colorectal cancer (MCC) samples. The gene is up-regulated in colon cancer-derived metastases compared to normal colon tissue. It is an example of claimed nucleic acid molecules that are up- or down-regulated in metastatic colorectal cancer cells. Such MCC-associated nucleic acids are useful in diagnostic and prognostic applications, in screening applications e.g. blochips, for identification of variant MCC-associated sequences, in informatics, for expression of MCC-associated proteins, in drug screening assays for identification of modulators of MCC-associated proteins, which are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting the growth or proliferation of a colon neoplasia in a subject, for treating colon cancer, comprises administering to the subject an agent that decreases the amount of a polypeptide present in or produced
                                                                                                                                                             for treating this cancer, in gene therapy, as \overline{DNA} vaccines, and as antisense or ribozyme modulators of MCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ColoUp5; colon cancer; marker; diagnosis; cytostatic; vaccine; gene therapy; FoxQ1; gene; ss.
                                                                                                                                                                                                            Sequence 1209 BP; 150 A; 485 C; 432 G; 141 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                         00000
                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                  242 GCTGCTGCCGGGATCGCCTCCTCCGCG 216
                                                                                                                                                                                                                                                                                                                                                                   US-09-989-890-238 (1-212) x ABQ81557 (1-1209)
                                                                                                                                                                                                                                                                                                                                                                                                  59 AlaAlaAlaGlyIleAlaSerSerAla 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .1209
/*tag= a
/product= "ColoUp5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCA-) UNIV CASE WESTERN RESERVE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-2002; 2002US-00229345.
27-AUG-2002; 2002US-0406296P.
18-OCT-2002; 2002US-00274177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-2003; 2003WO-US027086
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9.00
100.0%
1.00.0%
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                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL70222;
                                                                                                                                                                                                                                                                                                                     Query Match:
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    88333333333338
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Claim 3; SEQ ID NO 9; 125pp; English

the colon neoplasia

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The present sequence is the nucleic acid sequence of ColoUps a molecular marker of colon neoplasia. ColoUps was identified by expression microarray profiling of genes showing differential expression in normal colon and metastatic colon cancer. ColoUps is referred to in the literature as FoxQl (Forkhead box subclass q, member 1, formerly known as HPH-1), which plays a role in tissue-specific gene regulation as development, cell cycle regulation, cell signalling and tumourigenesis. The molecular marker is useful in the detection or diagnosis of colon neoplasia and for categorising the neoplastic state of a patient. Methods for inhibiting the growth or proliferation of a colon neoplasia involve the use of short interfering RNA (siRNA) or antisense oligonucleotides, can an agent that binds to and antagonises the polypeptide. Molecular markers can also be used to taxget therapeutic agents to cells of a colon neoplasia, and to screen and identify candidate therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel molecular markers for categorizing the neoplastic state of a patient. The invention further comprises a method for detecting whether a subject is likely to have a colon neoplasia. The method comprises: obtaining a biological sample from the subject; detecting one or more polypeptides selected from among: one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecular marker; neoplastic state; colon neoplasia; ColoUp1; ColoUp2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting likeliness of subject to have colon neoplasia, involves obtaining biological sample from subject, detecting one or more of ColoUpl and ColoUp2 polypeptides, presence of polypeptide indicating
                                                                                                                                                                                                                                                                                                    Sequence 1209 BP; 150 A; 485 C; 432 G; 141 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colon neoplasia ColoUp5 nucleic acid, SEQ ID No 9.
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AlaAlaAlaGlyIleAlaSerSerAla 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ IDS 1850-9691 represent a set of about 7842 genes or partial genes from the genome of the bacterium Mxyococcus xanthus. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
Coloupl polypeptides and one or more Coloup2 polypeptides, wherein the presence of said one or more polypeptides is indicative of colon neoplasia. The invention further comprises a kit for carrying out the said method. The methods and compositions are useful for detecting colon cancer. This polynucleotide sequence represents the Coloups gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic plant; DNA replication; gene regulation; gene expression;
                                                                                                                        Seguence 1209 BP; 150 A; 485 C; 432 G; 141 T; 0 U; 1 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutations in a gene of interest.
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                                                                                      invention.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 72008.
                        Conservative:
Mismatches:
Indels:
        Length:
Matches:
                                                                                                    1289 AGTGCCAGCGCGCTGCGGAATCGCT 1263
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                                                                                         56 SerAlaSerAlaAlaGlyIleAla 64
                                                      Gaps:
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                         Percent Similarity:
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  da; gene; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nontropic; neuroprotective; antibacterial; virucide; fungicide; opthalmological; gene therapy; channel/transporter protein; rheumatoid arthritis; neoplasm; cardiac arrest; cerebrovascular disorder; cerebral ischemia; angiogenesis; nervous system disorder; Alzheimer's disease; ocular disorder; corneal infection; wound healing; epithalial cell proliferation; skin aging; sunburn; transplantation; chemotaxis; food additive.
        Conservative:
Mismatches:
Indels:
  Matches:
                                                                                                                                                                                                  Novel human channel/transporter gene #223.
                                                                            US-09-989-890-238 (1-212) x AAC52650 (1-1436)
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02-MAR-2000;
16-MAR-2000;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule encoding a channel/transporter protein or sequences at least 95% identical to a these. The nucleic acids and proteins encoded by them are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used to dispin such a pathological condition or susceptibility to a cast of pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic in alleviating symptoms associated with the disorders and in diagnostic memunoscasays or enzyme linked immunosorbent assays (BLISA). Disorders which are diagnosed or treated immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. corporating carrest, cerebrovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. or cracial infections caused by arrest, or truses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial call proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in Chemotaxie. The polypeptides can also be used as a food additive or preservative to increase or decrease contact the corporation of the preservative to increase or decrease encorporation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a channel/transporter protein is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 233; 809pp; English
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P-PSDB; ADM19905.
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Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzhelmer's disease; AIDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointeetinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukemia; neovascularisation; erspiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy; gene; ss.
                                                                                                                                             DNA encoding novel central nervous system protein #169.
             157 TTGCCATCCTCTCTGGCCTTGTTGTCC 183
24 LeuProSerSerLeuAlaLeuLeuSer 32
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Rosen CA, Barash SC, Ruben SM (HUMA-) HUMAN GENOME SCI INC.

WPI; 2001-581633/65. P-PSDB; AAU87259.

New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 1; SEQ ID NO 179; 837pp; English

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (II), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, system disorders e.g. cardiac arrest, orelarial solates in anylogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fundi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. disphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders e.g. nonallargatic rhinitis, renal disorders e.g. caute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and ceptimal organs before transplantation, for supporting cell culture of primary tissues. to regenerate tissues and in chemotaxis. The collin, protein, coprimary tissues can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Alignment Scores:			
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meuroprotective; nootropic; antiparkinsonian; anticonvulsant;
antidiabetic; antirheumatic; antiarthritic; dermatological;
antiinflammatory; immunosuppressive; antithroid; antianemic; vasotropic;
anti-HIV; hepatotropic; virucide; antithroid; antianemic; vasotropic;
anti-HIV; hepatotropic; virucide; antithroid; antiantiale;
antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
artiovascular; antiarteriosclerotic; antiartrythmic; cardiant;
nephrotropic; litholytic; cytostatic; gene therapy; neural disorder;
nephrotropic; lateral sclerosis; multiple sclerosis;
amyotrophic lateral sclerosis; multiple sclerosis;
immune system disorder; diabetes; rheumatoid arthritis;
systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anaemia;
inflammatory disorder; ischemenia-reperfusion injury;
inflammatory bowel disease; Crohn; disease; infectious disease;
HIV infection; hepatitis infection; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                        fungal infection; parasitic infection; muscular disorder;
reproductive disorder; gastrointestinal disorder; pulmonary disorder;
cardiovascular disorder; atherosclerosis; arrhythmia; myocarditis;
renal disorder; acute glomerulomephritis; pyelonephritis;
renal lithiasis; proliferative disorder; cancerous diseases; human; gene;
                                                                                                                                                                     cDNA encoding novel human protein seq id 179.
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                                                                                                                                                22-APR-2004 (first entry)
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 - JUN - 2000;
30 - JUN - 2000;
07 - JUL - 2000;
07 - JUL - 2000;
11 - JUL - 2000;
14 - JUL - 2000;
26 - JUL - 2000;
26 - JUL - 2000;
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14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                         ADI53976;
                                                                           RESULT 46
                                                                                        ADI53976
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The invention describes an isolated polypeptide comprising an amino acid sequence at least 90% identical to: a polypeptide fragment, domain, epitope, or full-length protein of any one of 607 amino acid sequences (I) described in the specification; a polypeptide fragment of (I), or the encoded sequence contained in (II), having biological activity; or a variant, allelic variant, or a species homologue of (I). The polypeptides and nucleic acid molecules are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides and nucleic acid molecules, useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medic conditions e.g. neural disorders, reproductive disorders or infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 179; 413pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash SC;
                                  2000US - 0246613P

2000US - 0249207P

2000US - 0249209P

2000US - 0249210P

2000US - 0249210P

2000US - 0249211P

2000US - 0249213P

2000US - 0249213P

2000US - 0249214P

2000US - 0249216P

2000US - 0249216P

2000US - 0249216P

2000US - 0249216P
                                                                                                                                                                                                                       2000US-0249245P.
2000US-0249264P.
2000US-0249265P.
2000US-0249297P.
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2000US-0249300P.
2000US-0250160P.
2000US-0250391P.
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2000US-0251988P.
2000US-0256719P.
2000US-0251479P.
                                                                                                                                                                                                                                                                                                                                                                                 200005-0251866P
200005-0251868P
200005-0251869P
200005-0251899P
2000015-0251990P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROSEN C A.
RUBEN S M.
BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-122079/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-122079/
P-PSDB; ADI54574.
                                  08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JAN-2001;
                                                                                                                                                                                                                                                                              17-NOV-2000;
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                                                                                                                                                                                                                                                                 17-NOV-2000;
                                                                                                                                                                                                                                                                                                                   01-DEC-2000;
                                                                                                                   NOV-2000;
                                                                                                                                17-NOV-2000;
                                                                                                                                            NOV-2000;
                                                                                                                                                         17-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ROSE/) 1
(RUBE/) 1
(BARA/) 1
                                                                                                                                                                                                             17-NOV-2
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medical

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1564
9
0
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0
      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                        Gaps:
      403
9.00
100.0%
100.0%
4.2%
                            Local Similarity:
                    Percent Similarity:
Alignment Scores:
Pred. No.:
                                Query Match:
DB:
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US-09-989-890-238 (1-212) x ADI53976 (1-1564)

disorder characterised by an absence of, inappropriate or unwa-expression of the protein. The sequence presented is the human transporter protein cDNA

Sequence 1644 BP; 389 A; 419 C; 374 G; 462 T; 0 U; 0 Other;

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the invention undertobe an isolated number to perpetation.

Its allelic variants or orthologues, number polymucleotides encoding them. Transporter proteins regulate many different functions of the cell, including cell proliferation, differentiation and signalling processes, by regulating the flow of molecules, such as ions and macromolecules, into and out of cells. The polymucleotide and polymeptide can be used to craise antibodies, create a gene chip, create a transperic can be used to animal, produce the novel polypeptide, detect the presence of the polypeptide or nucleic acid in a sample, identify a modulator of the polypeptide or the expression, identify a pharmaceutical composition, and carrier, that binds to the polypeptide and treat a disease or condition mediated by a human transporter protein which comprises administering to mediated by a human transporter protein which comprises administering to a patient the composition in the development of human therapeutics and diagnostic compositions. The peptides are also useful for eliciting an immune response, to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids or as markers for tissues in which the corresponding protein is preferentially expressed. The agents identified are useful for treating to the agents identified are useful for treating to conditions and a modulator of the peptide is also useful for treating a disorder characterised by an absence of, inappropriate or unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human transporter proteins, useful for developing therapeutic or diagnostic compositions, particularly for developing human therapeutic agents that modulate transporter activity in cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention discloses an isolated human transporter polypeptide, and
                                                                                                                                                                                                                                                                         Human, gene, ss; transporter protein; allelic variant;
cell proliferation; cell differentiation; cell signalling; antibody;
gene chip; transgenic; therapeutic; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Transporter protein"
                          TTGCCATCCTCTGGCCTTGTTGTCC 182
LeuProSerSerLeuAlaLeuLeuSer 32
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                     ВЪ
                                                                                                                                                                                                                                      Human transporter protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 1; 129pp; English
                                                                                                                   ABS56295 standard; cDNA; 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2002; 2002WO-US000456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JAN-2001; 2001US-0262658P
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200279252-A1
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                             17-JAN-2003
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                                                                                                                                                          ABS56295;
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                                  셤
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8 셤

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The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest, and for constructing mutations in a gene set of about 7842 genes or partial genes from the genome of the bacterium Mxyococcus xanthus. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                                                                                                                             Transgenic plant; DNA replication; gene regulation; gene expression;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 1716 BP; 230 A; 580 C; 660 G; 246 T; 0 U; 0 Other;
           1644
0
0
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0
             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                       1511 TTGCCATCCTCTGGCCTTGTTGTC 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 9034; 25pp; English.
                                                                                                                         (1-1644)
                                                                                                                                                        24 LeuProSerSerLeuAlaLeuLeuSer 32
                                                                                                                                                                                                                                                                                                                                                 M. xanthus gene sequence, seq id 9034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Slater SC,
                                                                                                                         US-09-989-890-238 (1-212) x ABS56295
                                                                                                                                                                                                                                  ACL72571/c
ID ACL72571 standard; DNA; 1716 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-2000; 2000US-0217883P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-2001; 2001US-00902540
                                        100.0%
100.0%
4.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldman BS, Hinkle GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-028716/03.
                                                                                                                                                                                                                                                                                                                                                                                                                            Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          directly from USPTO
                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6833447-B1.
Alignment Scores:
                                                                                                                                                                                                                                                                                                                02-JUN-2005
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                                                                                                                                                                                                                                                                                   ACL72571;
                  :.
9
                                                                                                                                                                                                                                                                                                                                                                                               gene;
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1716 9 0 0 0

Length: Matches: Conservative: Mismatches: Indels:

439 9.00 100.0% 4.2%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

Gaps:

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The present invention provides the protein and coding sequences of a number of human transporter and ion channel proteins, designated TRICH-1-TRICH-3. The sequences can be used in the treatment of transport, neurological, muscle, immunological and cell proliferative disorders. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human transporters and ion channel polypeptides for diagnosing, treating or preventing transport, neurological, muscle, immunological and
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; transporter and ion channel; TRICH; transport disorder; eurological disorder; muscle disorder; immunological disorder; cell proliferative disorder; neuroprotective; nootropic; erebroprotective; immunosuppressive; cytostatic; respiratory; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lal P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y, Lal P
Khan FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;
Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang J;
Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;
Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azimzai Y, Lal
Blliott VS, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan FA;
Kearney L, Thangavelu K, Das D, Policky JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1818 BP; 435 A; 455 C; 417 G; 511 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                               Human transporter and ion channel TRICH-29 cDNA.
                                                                                     Indels:
US-09-989-890-238 (1-212) x ACL72571 (1-1716)
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                                                      SerGlyAlaGlyLeuProSerAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 227; 230pp; English.
                                                                                                                                                                                                               AAL44695 standard; 'cDNA; 1818 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell proliferative disorders.
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14-JUL-2000; 2000US-0218232P.
21-JUL-2000; 2000US-022112P.
28-JUL-2000; 2000US-0221839P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2001; 2001WO-US021448
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                                                                                                                                                                                                                                                                                                                           03-MAY-2002 (first entry)
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Best Local Similarity:
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The present invention relates to a nucleic acid molecule encoding a UST3-LIKE1 or its regulator is useful for the treatment of gastrointestinal and liver diseases, metabolic diseases, hematological disorders, respiratory diseases, neurological disorders, usological disorders and cardiovascular diseases in a mammal. The regulator is a man and molecule, an RNA molecule, an antisease oligonucleotide, a polypeptide, an antishody, or a ribozyme. The disorders include liver cirrhogis, liver tumours, achalasia, dysphagia, gastroesophageal reflux, diabetes, crohn's disease, diarrhes, constipation, osteoporosis, Alzheimer's disease, Parkinson's disease, anemia, leukemia, lymphomas, asthma, allergies, stroke, dementia and arrhythmias. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule encoding an organic anion transporting (OAT)-
like protein UST3-LIKE1, useful for treating gastrointestinal, metabolic,
respiratory, neurological and cardiovascular diseases.
                                                                                                                                                                                                                       UST3-LIKEI; Hepatotropic; Antiinflammatory; Cytostatic; Antidiabetic; Cardiant; Hemostatic; Vasotropic; Osteopathic; Antiparkinsonian; Antianemic; Laxative; Antidiarrheic; Antiasthmatic; Antiallergic; Cerebroprotective; antiarrhythmic; gastrointestinal; cirrhosis; tumour; Alzheimer's disease; Parkinson's disease; anemia; leukemia; lymphomas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1912 BP; 495 A; 461 C; 413 G; 543 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents UST3-LIKE1 protein encoding sequence.
1685 TIGCCATCCTCTGGCCTTGTTGTCC 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "UST3-LIKE1"
                                                                                                                                                                                        UST3-LIKE1 protein encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
61. .1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Geerts A;
                                                                                                                                                                                                                                                                                                                         asthma; dementia; arrhythmias; ss.
                                                                          ADR86567 standard; cDNA; 1912 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-2004; 2004WO-EP002172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-2003; 2003EP-00004939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FARB ) BAYER HEALTHCARE AG.
                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brueggemeier U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-677521/66.
P-PSDB; ADR86568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004081041-A1.
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                     16-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                               ADR86567;
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Length:
Matches:
Conservative:
Mismatches:
Indels:

485 9.00 100.0% 100.0% 4.2%

> Percent Similarity: Best Local Similarity:

Gaps: (1-1912)

US-09-989-890-238 (1-212) x ADR86567

24 LeuProSerSerLeuAlaLeuLeuSer 32

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ransporters and ion channel; TRICH; neuroprotective; relaxant;

antithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive;

antithiammantory; thyromimetic; antiallergic; cerebroprotective;

gastrointestinal; hepatotropic; antiparasitic; dingicide; protozoacide;

w irucide; uropathic; antirheumatic; cardiant; cardionvulsant;

noctropic; TRICH agonist; TRICH antiparasitic; fungicide; protozoacide;

w muscular disorder; myotonic dystrophy; catatonis, endocrine disorder;

muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;

breast cancer; immunological disorder; scarodarm;

systemic lupus erythematosus; allergy; gastrointestinal disorder;

crohis disease; renal disorder; Goodpasture's syndrome; infection;

viral; bacterial; fungal; parasitic; protozoal; helminthic;

cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel human transporters and ion channel (TRICH) proteins and the nucleotide sequences which encode them. The invention may be useful for the production of compounds with a neuroprotective, relaxant, antithyroid, antidiabetic, cytostatic, dermatological, immunosuppressive, autiinflammatory, thyromimetic, antiallergic, creebroprotective, gastrointestinal, hepatotropic, nephrotropic, anticonvulsant, antiparkinsonian, antibacterial, antiparsitic, fungicide, protozoacide, virucide, uropathic, antitheumatic, cardiant, cardiant, cardiant, anti-HIV or nootropic activity acting as TRICH agonists or antagonists. In addition the disclosed sequences may be useful for gene therapy. The invention may be useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hafalia AJA, Khare R, Lal PG, Yue H, Baughn MR, Thornton MB; Lu DAM, Ison CH, Becha SD, Ding L, Warren BA, Lee SY, Swarnakar A; Elliott VS, Richardson TW, Marquis JP, Ramkumar J, Murage J; Raumann BE, Yao MG, Lu Y, Gietzen KJ, Yang YG, Chang H, Chawla NK; Tran UK, Lee S, Yang J, Gandhi AR, Tribouley CM, Policky JL; Ring HZ, Lee EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New TRICH polypeptides, useful for diagnosing, preventing, and treating disorders associated with abnormal expression or activity of TRICH, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or
                                                                                                                                                                                                                                 Human transporter and ion channel (TRICH) gene SegID57.
1589 TTGCCATCTTTTTGTTGTTGT 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 57; 285pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic animal; gene; ds; human.
                                                                                                       ADN33172 standard; DNA; 1960 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002US-0419313P.
2002US-0421033P.
2002US-0421349P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2003; 2003WO-US033087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-2002; 2002US-0423516P
                                                                                                                                                                                          18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-348448/32.
P-PSDB; ADN33116.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004035755-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2002;
23-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infections.
                                                                                                                                                 ADN33172;
                                                              RESULT 51
                                                                                    ADN33172
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diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of TRICH, such as neurodegenerative disorders (for example Parkinson's disease, Alzheimer's disease), muscular disorders (for example myotonic dystrophy, catatonia), endocrine disorders (for example diabetes, Grave's disease), cancers (for example eleukaemia, carvical or breast cancers), immunological disorders (for example electoderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (for example Crohn's disease), renal disorders (for example Goodpasture's syndrome), infections (for example viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (for example atherosclerosis), or hepatic diseases (for example cirrhosis); TRICH or its fragments may also be used in screening for compounds that specifically bind to and modulate the activity of TRICH. The nucleotides can be used to create humanised animals or transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animals to model human disease. The present sequence is that of a human transporter and ion channel (TRICH) gene of the invention.
      888888888888888888
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Sequence 1960 BP; 457 A; 512 C; 448 G; 543 T; 0 U; 0 Other;

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1960
9
0
0
0
      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                            Gaps:
                                                            US-09-989-890-238 (1-212) x ADN33172 (1-1960)
       496
9.00
100.0%
4.2%
                             Best Local Similarity:
                      Percent Similarity:
Alignment Scores:
                                      Query Match:
                                                                                                           RESULT 52
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                                                                             ઠે
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ADS47648/c ID ADS47648 standard; cDNA; 2071 BP ADS47648;

02-DEC-2004 (first entry)

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; of account tolerance; pest tolerance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polymucleotide; gene; 88. Bacterial polynucleotide #2391.

US2003233675-A1.

18-DEC-2003.

20-FEB-2003; 2003US-00369493

21-FEB-2002; 2002US-0360039P CAOY/)

CAO Y. HINKLE G J. SLATER S C. CHEN X SLAT/) HINK/) CHEN/

GOLDMAN B S

(dolla)

Goldman BS; Chen X, Hinkle GJ, Slater SC, Cao Y,

WPI; 2004-061375/06.

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a

Homo sapiens

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypoptide from a microbial source. The invention alos relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant baving an improved property. The plant is a crop plant cancer and growing at pransformed plant to such as maize or soybean. The method of producing a transformed plant to excombinant DNA construct and growing the transformed plant with the polymucleotide or polypeptide is useful for improving plant with the compinant DNA construct is useful for improving plants with construct is useful for improving plants with construct is useful for producing plants with construct properties, e.g. improved plant properties, e.g. improved cold, heat or a drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or peats, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved light production of photosynthesis or by providing improved light production or improved galactomannan condition, improved light production or improved data for this patent did the scope of the invention. Note: The sequence cata for this patent did cont form part of the printed specification but was obtained in electronic format from USPTO at sequence. The sequence cata for this patent did contains.
microbial source, useful for producing plants with improved properties.
                                                                Claim 1; SEQ ID NO 26078; 122pp; English.
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Seguence 2071 BP; 608 A; 350 C; 429 G; 684 T; 0 U; 0 Other;

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00000
          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                    1572 GICTIAGIAGCCCCTCGAAGCACGAIT 1546
                                                            Indels:
                                                                                                                       175 ValLeuValAlaProArgSerThrile 183
                                                                                                US-09-989-890-238 (1-212) x ADS47648 (1-2071)
                                                                                                                                                                                               ADN33202 standard; DNA; 2238 BP.
                                                                                                                                                                                                                                              18-NOV-2004 (first entry)
                                 100.08
100.08
4.28
13
           522
9.00
                                                Best Local Similarity:
                                   Percent Similarity:
Alignment Scores:
                                                                                                                                                                                                                       ADN33202;
                                                         Query Match:
DB:
                                                                                                                                                                        RESULT 53
                                                                                                                                                                                      ADN33202
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Transporters antidiabetic; cytostatic; dermatological; immunosuppressive; antidithyroid; antidiabetic; cytostatic; dermatological; immunosuppressive; antiditammatory; thyromimetic; antialergic; cerebroprotective; antidiabeticip; antidiabetic; cardiant; antidorus; transporters and ion channel; TRICH; neuroprotective; relaxant; Human transporter and ion channel (TRICH) gene SegID87. 2078 TIGCCALCCICICIGGCCTIGITGICC 2104

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This invention relates to novel human transporters and ion channel

(TRICH) proteins and the nucleotide sequences which encode them. The

invention may be useful for the production of compounds with a

curvention may be useful for the production of compounds with a

neuroprotective, relaxant, antithyroid, antidiabetic, cytostatic,

dermatological, immunosuppressive, antiinflammatory, thyromimetic,

cardial cardiant, cardiant, antiparkinsonian, antibacterial,

matiparasitic, fungicide, protozoacide, virucide, uropathic,

antiparasitic, cardiant, cardiavascular, anti-HIV or nootropic,

antiparasitic, cardiant, cardiavascular, anti-HIV or nootropic,

antiparasitic, cardiant, cardiavascular, anti-HIV or nootropic,

acting as TRICH agonists or antagonists. In addition the disclosed

carding as reventing, and treating disorders associated with an

cappormal expression or activity of TRICH, such as neurodegenerative

cappormal expression or activity of TRICH, such as neurodegenerative

cappormal expression or activity of disease, Alzheimer's disease),

capporders (for example parkinson's disease, Alzheimer's disease),

capporders (for example myotonic dystrophy, cardional, endocrine

disorders (for example diabetes, grave's disease), cancers (for

example soleroderma, systemic lupus erythematosus, allergies),

capporders (for example atheroselerosi), immunological disorders

(for example Goodpasture's syndrome), infections (for example viral,

capporders (for example atheroselerosis), or hepatic diseases (for example

carrhosis). TRICH or its fragments may also be used in screening for

cirrhosis). TRICH or its fragments may also be used in screening for

compounds that specifically bind to and modulate the activity of TRICH.

The nucleotides can be used to create humanised animals to a human

compounds the present sequence is that of a human

compounds the present sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                        Hafalia AJA, Khare R, Lal PG, Yue H, Baughn MR, Thornton MB;
Lu DAM, Ison CH, Becha SD, Ding L, Warren BA, Lee SY, Swarnakar A;
Elliott VS, Richardson TW, Marquis JP, Ramkumar J, Murage J;
Raumann BE, Yao MG, Lu Y, Getezen KJ, Yang YG, Chang H, Chawla NK;
Tran UK, Lee S, Yang J, Gandhi AR, Tribouley CM, Policky JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New TRICH polypeptides, useful for diagnosing, preventing, and treating disorders associated with abnormal expression or activity of TRICH, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2238 BP; 547 A; 563 C; 506 G; 622 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; SEQ ID NO 87; 285pp; English.
                                                                                                                                                               2002US-0419313P.
2002US-0421033P.
2002US-0421349P.
                                                                                                            16-OCT-2003; 2003WO-US033087.
                                                                                                                                                                                                                                               04-NOV-2002; 2002US-0423516P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-348448/32.
                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tran UK, Lee S,
Ring HZ, Lee EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ADN33146.
WO2004035755-A2
                                                                                                                                                                  16-OCT-2002;
                                                                                                                                                                                                                        25-OCT-2002;
                                                      29-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infections.
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Alignment Scores:

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2238
9
0
0
0
Length:
Matches:
Conservative:
Mismatches:
Indels:
 561
9.00
100.0%
100.0%
4.2%
                       Best Local Similarity:
               Percent Similarity:
                             Query Match:
DB:
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US-09-989-890-238 (1-212) x ADN33202

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LeuProSerSerLeuAlaLeuLeuSer 32
        24
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AAS79799/c

RESULT 55

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The present invention provides the protein and coding sequences of a number of human transporter and ion channel proteins, designated TRICH-1-TRICH-32. The sequences can be used in the treatment of transport, neurological, muscle, immunological and cell proliferative disorders. The present sequence is a coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human transporters and ion channel polypeptides for diagnosing, treating or preventing transport, neurological, muscle, immunological and cell proliferative disorders.
                                                                                                                                                                                                                                                        Human; transporter and ion channel; TRICH; transport disorder; neurological disorder; muscle disorder; immunological disorder; cell proliferative disorder, neuroprotective, nootropic; cerbroprotective; immunosuppressive; cytostatic; respiratory; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L;
Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Khan FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;
Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang
Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;
Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azinzai Y,
Elliott VS, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2245 BP; 550 A; 559 C; 491 G; 645 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2245
0 0 0
0 0 0
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Mismatches:
Indels:
                                                                                                                                                                                                       Human transporter and ion channel TRICH-30 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu Y, Seilhamer JJ,
, Das D, Policky JL;
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2112 TTGCCATCCTCTCTGGCCTTGTTGTCC 2138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-989-890-238 (1-212) x AAL44696 (1-2245)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 228; 230pp; English.
                                              AAL44696 standard; cDNA; 2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-2000; 2000US-0216547P.
14-JUL-2000; 2000US-0218232P.
21-JUL-2000; 2000US-0220112P.
28-JUL-2000; 2000US-0221839P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2001; 2001WO-US021448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nguyen DB, X
Thangavelu K,
                                                                                                                                                     03-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563
9.00
100.0%
100.0%
                                                                                                                                                                                                                                                                                                                                                                     gene therapy; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AA014213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200204520-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elliott VS,
Kearney L,
                                                                                                    AAL44696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
DB:
RESULT 54
                        AAL44696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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Lal P;

ACN43045 standard; cDNA; 2275 BP.

ACN43045/

ACN43045;

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed centry of (II) as useful in gene therapy techniques to restore normal certivity of (II) or to tread disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging convolving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, foresists, generations in displance other types of data and products dependent on DNA and the produce other types of data and products dependent on DNA and the produce of the types of data and products dependent on DNA and the produce of the types of data and products dependent on DNA and the produce of the types of data and products dependent on DNA and the produce of the types of data and products dependent on DNA and the produce of the types of data and products dependent on DNA and the produce of the types of data and products dependent on DNA and the products dependent on DNA a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2256 BP; 487 A; 771 C; 609 G; 389 T; 0 U; 0 Other;
                                                                                                                                                                        DNA encoding novel human diagnostic protein #15603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 15603; 103pp; English.
AAS79799 standard; cDNA; 2256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABG15612
                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                               13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2001
                                                      AAS79799;
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Alignment Scores:

directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 2275 BP; 472 A; 691 C; 624 G; 488 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels:

570 9.00 100.0% 1.00.0%

Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores: Pred. No.:

Gaps:

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Conservative:
Mismatches:
Indels:
Gaps:
Length:
Matches:
                                                                                                                           337 CTTCCTTCAGCGTCAGCAGCAGCTGGA 311
                                                                                   US-09-989-890-238 (1-212) x AAS79799 (1-2256)
                                                                                                           54 LeuProSerAlaSerAlaAlaGly 62
565
9.00
100.0$
4.2$
                                     Local Similarity:
                        Percent Similarity:
                                              Query Match:
DB:
                                                                                                           8
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, dastrointestinal disorder, or consecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline to gene therapy. The present sequence represente a dithp polymorleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gietzen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.
                                                                                                                                   gene; gene therapy; human diagnostic and therapeutic polynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panezer SK, Wang X, Au AP, Gerstin EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES; Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletze Patury S, Shi X, Suarez CJ;
                                                                                              Human diagnostic and therapeutic polynucleotide SEQ ID NO:1920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 190pp; English.
                                                                                                                                                                                                                                                                                                                     12-SEP-2003; 2003WO-US028227.
                                                                                                                                                                                                                                                                                                                                                             12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
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                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE CORP
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                                                                                                                                                                                                  Homo sapiens.
                                                    18-NOV-2004
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RESULT 5'

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                      Drosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5906 BP; 1234 A; 1501 C; 1649 G; 1522 T; 0 U; 0 Other;
                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 4885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 4885; 21pp + Sequence Listing; English
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Matches:
Conservative:
Mismatches:
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11-JUL-2000; 2000US-00614150
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genes from Drosophila and
                                    (first entry)
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                                                                                                                           pharmaceutical; gene; ds.
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                                                                                                                                                             Drosophila melanogaster.
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interactions.
                                    26-MAR-2002
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ABL17804;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                      Drosophila melanogaster genomic polynucleotide SEQ ID NO 4888.
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Matches:
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US-09-989-890-238 (1-212) x ACN43045 (1-2275)
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                                    ProSerSerLeuAlaLeuLeuSerArg 33
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ABL17804/c
ID ABL17804 standard; DNA; 5906 BP.
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity:
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5906 9 0 0 0

Myxococcus xanthus

Query Match

Score:

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2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
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                                                                                             2000US-0209467P
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2000US-0216880P.
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02-OCT-2000;
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19-MAY-2000;
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08-SEP-2000;
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                                             16-MAR-2000;
17-MAR-2000;
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22-AUG-2000;
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The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest sequences given in records for SEQ IDs 1-1849 represent a set of 1849 contig and singleton sequences comprising coding sequences, the genements, promoters and other regulatory elements from the geneme of the bacterium Mayococcus xanthus. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                              New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic sequence #367 encoding for novel human respiratory antigen.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7874 BP; 1293 A; 2530 C; 2661 G; 1390 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                 Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;
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                                                                                                                                                                                                                       Example 1; SEQ ID NO 868; 25pp; English.
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                                                                                          (MONS ) MONSANTO TECHNOLOGY LLC
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                                             10-JUL-2001; 2001US-00902540
                                                                    10-JUL-2000; 2000US-0217883P.
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US6833447-B1
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                       21-DEC-2004
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The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, consillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose clisorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
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Matches:
Conservative:
Mismatches:
Indels:
              Disclosure; SED ID No 961; 546pp; English
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AAS28526 standard; DNA; 7880 BP.
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2000US-018464P.
2000US-0186350P.
2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
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2000US-0217487P
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Query Match:
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18-APR-2000;
19-MAY-2000;
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16-MAR-2000;
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Barash SC, Ruben (HUMA-) HUMAN GENOME SCI INC Rosen CA,

WPI; 2001-476224/51.

prognosing respiratory cancers Isolated polypeptide for treating, preventing and/ or disorders related to the respiratory system including and also for testing and detection e.g. diagnosis.

Disclosure; SED ID No 960; 546pp; English.

The present invention relates to the isolation of novel human respiratory antigens (AAU17685-AAU17975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the tonsillitis, and laryngitis), lung disorders e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS2876 represent genomic sequences encoding for novel human respiratory antigens. Note: The sequence encoding for more form part of the printed specification, but was obtained in electronic format directly from WIPO at

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20-0CT-2000;
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02-OCT-2000;
02-OCT-2000;
 respiratory system antigen; human respiratory systems associated polynucleotide; respiratory system associated polynucleotide; respiratory system disorder; throad disorder; vocal cord paralysis; tonsillitis; laryngitis; lung disorder; preumonia; allergic disorder; asthma; eosinophilic pneumonia; pleurisy; cystic fibrosis; emphysema; histiccytosis; sarcoidosis; nose disorder; rhinitis; sinusitis; neoplasm; cancer; respiratory tissue cancer; throat cancer; lung cancer; cancer; lung cancer; human respiratory system associated protein; ds; human.
                                                                                                                                                                                                                                                                                                antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
                   Sequence 7880 BP; 1588 A; 2333 C; 2091 G; 1868 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                           Human respiratory system associated genomic DNA seg id 961.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ftp.wipo.int/pub/published_pct_sequences
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DB:
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techniques, for chromosome identification, identifying individuals from

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The invention describes an isolated polypeptide (I) comprising an amino acid sequence that is at least 90% identical to polypeptide fragment of any one of 299 respiratory system antigen sequences (PS) and having biological activity, polypeptide domain or epitope of PS, full-length protein of PS, or variant, alledic variant or species homolog of PS. (I) cr a polymucleotide (II) encoding (I) is also useful for diagnosing a pathological condition or a uscreptibility to a pathological condition in a subject which involves determining the presence or absence of mutation in a subject which involves determining the presence or absence of mutation in (II) or determining the presence or amount of expression of (I) in a biological sample and diagnosing a pathological condition based on the result. The human respiratory system associated polynucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides are useful in diagnosis, treatment, prevention and/or prognosis of disorders of respiratory system such as throat disorders (e.g., pneumonia), allergic disorders, (e.g., asthma and eosinophilic pneumonia), pleurisy, cystic fibrosis, emphysema, histicoyfosis, pneumonia), pleurisy, cystic fibrosis, emphysema, histicoyfosis, sarcoidosis, nose disorders (thinitis and larymoitis), neoplasms and/or cancers of respiratory tissues (e.g., throat cancer, lung cancer, and cancer of the nose). The polymucleotides are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel respiratory system antigen and polynucleotides encoding the polypeptides, useful for treating diagnosing, treating or preventing tonsillitis, pneumonia, asthma and cystic fibrosis, emphysema, throat
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respiratory system antigen; human respiratory system associated polynucleotide; respiratory system associated polynucleotide; cord paralysis; respiratory system disorder; throad disorder; vocal allergic disorder; ensillitis; laryngitis; lung disorder; pneumonia; allergic disorder; asthma; eosinophilic pneumonia; pleurisy; cystic fibrosis; emphysema; histlocytosis; sarcoidosis; nose disorder; rhinitis; sinusitis; neoplasm; cancer; respiratory tissue cancer; throat cancer; lung cancer; cancer of the nose; gene therapy; chromosome identification; forensic; human respiratory system associated protein; ds; human.
                                                                                                                                                                                                                                                                                                          antiinflammatory, antiallergic; antiasthmatic; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                 Human respiratory system associated genomic DNA seq id 960.
           7880
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Matches:
Conservative:
                                                 Mismatches:
Indels:
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM, Barash SC;

WPI; 2003-902033/82.

Novel respiratory system antigen and polynucleotides encoding the polypeptides, useful for treating diagnosing, treating or preventing tonsillitis, pneumonia, asthma and cystic fibrosis, emphysema, throat cancer.

Disclosure; SEQ ID NO 960; 236pp; English.

The invention describes an isolated polypeptide (I) comprising an amino acid sequence that is at least 90% identical to polypeptide fragment of any one of 299 respiratory system antigen sequences (PS) and having biological activity, polypeptide domain or epitope of PS, full-length biological activity, polypeptide domain or species homolog of PS. (I) cordition or a susceptibility to a pathological condition in a subject which involves determining the presence or absence of mutation a subject which involves determining the presence or absence of mutation or a subject which involves determining the presence or absence of mutation or a subject which involves determining the presence or absence of mutation or a subject which involves determining the presence or absence of mutation or a subject which involves determining the presence or absence of mutation or cault. The human respiratory system associated polymucleotides, the creatiff of diagnosing a pathological condition based on the result. The human respiratory system associated polymucleotides, the collypeptides are useful in diagnosis, treatment, prevention and/or these polypeptides are useful in diagnosis, treatment, prevention and/or prognosis of disorders of respiratory system such as throat disorders (e.g., pneumonia), allergic disorders, (e.g., asthma and ecosinophilic pneumonia), pleurisy, cystic fibrosis, emphysema, histiocytosis, arcoidosis, nose disorders (rhinitis and sinusitis), neoplasms and/or cancers of respiratory tissues (e.g., throat cancer, lung cancer, and cancers of the nose). The polymucleotides are useful in gene therapy techniques, for chromosome identification, identifying individuals from

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 respiratory system-related polypeptide, antiasthmatic, antibacterial, antiinflammatory; cytostatic; antianaemic; antiallergic; gene therapy; pneumonia; lung cancer; cystic fibrosis; asthma; sarcoidosis; rhinitis; anaemia; leukaemia; inflammation; sinustis; chronic obstructive pulmonary disease; infectious disease; human; ds.
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Conservative:
Mismatches:
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respiratory system-related polypeptide; antiasthmatic; antibacterial; antiinflammatory; cytostatic; antianaemic; antiallergic; gene therapy; pneumonia; lung cancer; cystic fibrosis; athma; sarcoidosis; rhinitis; anaemia; leukaemia; inflammation; sinustits; chronic obstructive pulmonary disease; infectious disease; human; ds.

Human respiratory system associated polypeptide-related DNA SeqID960

ADI97496 standard; DNA; 7880 BP.

04-NOV-2004 (first entry)

ADI97496;

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RESULT 65
ADI97496/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention is related to a novel isolated polypeptide, which comprises a human respiratory system-related polypeptide, and the DNA sequence which encodes it. The invention may be useful for the sequence which encodes it. The invention may be useful for the development of compounds with an antisathmatic, antibacterial, antibitation, the sequences disclosed may be useful for gene therapy. The polypeptide or polymouleotide is useful for treating, preventing or polypeptide or polymouleotide is useful for treating, preventing or medical condition, for example pneumonia, lung cancer, cystic fibrosis, asthma, sarcoidosis, rhinitis, anaemia, leukaemia, inflammations, sinusitis, chronic obstructive pulmonary disease or inflammations, sinusitis, chronic obstructive pulmonary disease or inflammations diseases. The polypeptide or polymorary disease or diseases. The polypeptide or polymorary disease. The disease or a susceptibility to the disease. The present sequence is that of a human DNA sequence which is related to a human respiratory system associated gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human respiratory system-related polypeptide and genes, useful for treating, preventing or diagnosing e.g. pneumonia, lung cancer, cystic fibrosis, asthma, sarcoidosis, rhinitis, leukemia, inflammations or sinusitis.
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24-APR-2003

Homo sapiens

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Mismatches:
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Percent Similarity: Best Local Similarity:

Query Match:

Gaps:

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This invention is related to a novel isolated polypeptide, which comprises a human respiratory system-related polypeptide, and the DNA sequence which encodes it. The invention may be useful for the development of compounds with an antiasthmatic, antibacterial, antiinflammatory, cytostatic, antianaemic or antiallergic activity. In addition, the sequences disclosed may be useful for gene therapy. The polypeptide or polymucleotide is useful for treating, preventing or ameliorating a medical condition, for example pneumonia, lung cancer, cystic fibrosis, astromic obstructive pulmonary disease or infectious diseases. The polypeptide or polymucleotide is also useful for infectious diseases. The polypeptide or polymucleotide is also useful for diagnosing any of these diseases or a susceptibility to the disease. The present sequence is that of a human DNA sequence which is related to a human respiratory system associated gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plant; DNA replication; gene regulation; gene expression; ds.
                                                                                                                                                                                                                                                                                                                                                                   New human respiratory system-related polypeptide and genes, useful for treating, preventing or diagnosing e.g. pneumonia, lung cancer, cystic fibrosis, asthma, sarcoidosis, rhinitis, leukemia, inflammations or sinusitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7880 BP; 1588 A; 2333 C; 2091 G; 1868 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 960; 202pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. xanthus DNA fragment, seq id 966.
                                                                                                                                                                                                                                                                                                       Barash SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACL64503 standard; DNA; 9198 BP
                                                                            2000US-0251988P.
2000US-0256719P.
                                                                                                          2000US-0251479P.
                                                                                                                                                        2000US-0251869P
                                                                                                                                                                                                          2000US-0254097P.
                                            2000US-0250391P
                                                                                                                                             2000US-0251868P
                                                               2000US-0251030P
                                                                                                                                                                                         2000US-0251990P
                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                        17-JAN-2001; 2001US-00764860
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                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                     WPI; 2003-765403/72.
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Best Local Similarity:
                                                             05-DBC-2000;
05-DBC-2000;
05-DBC-2000;
06-DBC-2000;
                                                                                                                         08-DEC-2000;
                                                                                                                                                          08-DEC-2000;
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DB:
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Novel genes which are differentially regulated in prostate cancer, usef for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

(ORIG-) ORIGENE TECHNOLOGIES INC.

WPI; 2003-058520/05. P-PSDB; ABU07489.

Jay G;

Sun Z,

06-APR-2001; 2001US-0281731P. 08-APR-2002; 2002WO-US010824

Claim 1; Page 140-144; 416pp; English.

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The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11956. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest. Sequences given in records for SEQ IDs 1-1849 represent a set of 1849 contig and singleton sequences comprising coding sequences, DNA replication elements, promoters and other regulatory elements from the genome of the bacterium Mayococcus xanthus. Note: The sequence data for this patent did not form part of the printed specification, but was
                                                                                                                                                                                                                                                         New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding protein differentially regulated in prostate cancer #63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9198 BP; 1247 A; 3175 C; 3389 G; 1387 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 966; 25pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGlyAlaGlyLeuProSerAlaSer 58
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                                                                                                                                                           (MONS ) MONSANTO TECHNOLOGY LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX10394 standard; DNA; 9771 BP
                                                                                               10-JUL-2001; 2001US-00902540.
                                                                                                                               10-JUL-2000; 2000US-0217883P.
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                                                                                                                                                                                           Goldman BS, Hinkle GJ,
                                                                                                                                                                                                                         WPI; 2005-028716/03.
 Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity:
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Best Local Similarit
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                               US6833447-B1
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                                                             21-DEC-2004
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corrections genes (1) with a section of the propagation of the number of prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of the probability that the sample comprises of target genes which are differentially regulated in the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves a subject having a prostate cancer, which involves cancer of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, staging, grading, assessing, monitoring, prognosticating, prognosticating, prognosticating, products are used in the diagnostic test to assay for presence of cancer conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer conditions especially relating for prostate cancer. (I) and its expression of cancer, its stage of development, the nature of genetic act.

The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus for specific genes, and groups of genes, expressed in pathways in pathways and disease pathways and the delineation of targets in these pathways which are useful in disease pathways and the delineation of targets in the app
                                                                                                                                                                                                                                                                                                                                                                                                           invention describes genes (I) which are differentially regulated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9771 BP; 3514 A; 2357 C; 2283 G; 1617 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
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ID ADI02721 standard; cDNA; 10432 BP.
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Best Local Similarity:
Query Match:
DB:
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mouse; murine; d
neuroblastoma; s
MYCN activated c
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DB:
                                                                                                                                                                                                                                                                                            cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a new combination which comprises cDNAs or their complements not given in the specification that are differentially expressed in vascular endothelium. The combination of cDNAs is useful for preparing a composition for diagnosing or treating vascular disorder, comprising atherosclerosis, haemangioma, haemangioendothelioma, oedema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy, warts, pyogenic granulomas, Kaposi's sarcoma, scar keloids, allergic oedema, neoplasms, pioriaals ulcers, follicular cysts, endometriosis, peritoneal sclerosis or obesity. The present sequence represents a cDNA differentially expressed in the vascular endothelium.
                                                                                                                                                                                                                                                                                                                                     New combination comprising cDNAs that are differentially expressed in vascular endothelium, useful for preparing a composition for diagnosing or treating vascular disorder, e.g., atherosclerosis, psoriasis, ulcers
                                                                             wart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine cDNA differentially expressed in MYCN activated cells SeqID 349.
                                         Human cDNA differentially expressed in the vascular endothelium #262
                                                              BB; vaBcular endothelium; vaBcular diBorder; atherosclerosis; haemangioma; haemangioendochelioma; oedema; diabetic retinopathy; wa pyogenic granuloma; Kaposi's Barcoma; BCar keloid; allergic oedema; neoplasm; pBoriasis; ulcer; follicular cyBt; endometriosis; peritoneal sclerosis; obesity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10432 BP; 3683 A; 2503 C; 2450 G; 1796 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 262; 28pp; English.
                                                                                                                                                                                                                                                                                           Cocks BG;
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                                                                                                                                                                                                                         27-APR-2001; 2001US-0287067P
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                      22-APR-2004 (first entry)
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                                                                                                                                                                                                                                                                                          Astromoff A, Bandman O,
                                                                                                                                                                                                                                             (ASTR/) ASTROMOFF A. (BAND/) BANDMAN O. (COCK/) COCKS B G.
                                                                                                                                                                                                                                                                                                                WPI; 2003-898115/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                        US2003166903-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                   Homo sapiens
                                                                                                                                                                              04-SEP-2003.
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DB:
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This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polymucleotida sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protonon cells activated by the transactivator MYCN, where MYCN is a protonon cogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polymucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an exemplification of the invention. NOTE: This sequence does not appear in the US Patent Office at
differential expression; transactivator; proto-oncogene; small cell lung cancer; cytostatic; gene therapy; ss; cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10432 BP; 3683 A; 2503 C; 2450 G; 1796 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA differentially expressed in a liver disorder #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                         25-FEB-2002; 2002US-00084817.
                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-2001; 2001US-0270784P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stuart SG, Nuchtern JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STUA/) STUART S G. (NUCH/) NUCHTERN J G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-635698/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PLON/) PLON S E. (SHOH/) SHOHET J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment represents a cDNA connective.
                                                                                                                                                                                                                                                                                                                                                                                                                Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 0 U; 0 Other;
               human; 88; gene; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 20; 41pp; English.
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                                                                                                                                                                                                                                                                                     (KASE/) KASER M R.
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                                                                                                                                          US2003108871-A1
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                                                                                                                                                                                                                                                                                                                             Kaser MR;
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DB:
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Human steroid-induced C3A liver cell cDNA #21.

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The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high troughput method of screening molecules or compounds to identify a throughput method of screening molecules or compounds to identify a wilson disease and comparison of a standard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at cast one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human cDNA which is differentially expressed in steroid-induced C3A liver calls. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                              Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNAs that are differentially expressed in response to steroid
                ss; gene; Hepatotropic; Gene therapy; Wilson disease; liver disorder; steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10432 BP; 3683 A; 2503 C; 2450 G; 1796 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA #75 differentially expressed in prostate cancer.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 21; 141pp; English.
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                                                                                                                                                                                        12-OCT-2001; 2001US-00976594.
                                                                                                                                                                                                                              12-OCT-2000; 2000US-0240409P
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9.00
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                                                                                                                                                                                                                                                                  (INCY-) INCYTE CORP.
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                                                                          Homo sapiens
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30-JUL-2001; 2001US-00919172
                                             28-JUL-2000; 2000US-0222469P
                                                                                               Faris M, Turner CM;
                                                                                                                 WPI; 2002-608155/65.
P-PSDB; ABG77188.
                                                                  (FARI/) FARIS M.
(TURN/) TURNER C M.
         29-AUG-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA64659;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a composition comprising cDNAs that are differentially expressed in prostate cancer. The composition is useful for diagnosing, staging or treating prostate cancer or for monitoring the treatment of a subject with prostate cancer. The invention is also used in gene therapy. The present sequence is the human cDNA differentially
                                                                                                                                                                                                                                                                            A composition comprising cDNAs that are differentially expressed in prostate cancer, useful for diagnosing, staging or treating prostate cancer or for monitoring the treatment of subjects with prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate cancer; differential expression; cancer diagnosis; cancer treatment; cancer monitoring; prostate adenocarcinoma; gene; ss.
                                                                         /*tag= a
/product= "Human protein differentially expressed in
prostate cancer"
marker; diagnostic; prostate cancer; cytostatic; gene therapy;
88.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10432 BP; 3683 A; 2503 C; 2450 G; 1796 T; 0 U; 0 Other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 97; 144pp; English.
                                                      Location/Qualifiers
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30-JUL-2001; 2001US-00919172.
                                                                                                                                                                                                                                                                                                                                                                                         expressed in prostate cancer.
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                                                                                                                                                                                                         (INCY-) INCYTE CORP
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DB:
         Tumor
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                                                        Key
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differentially expressed in prostate cancer. The composition of the invention useful for a high-throughput method for detecting differential expression of cDNAs in a nucleic acid containing sample comprising amplifying the nucleic acids of the sample, hybridishing the composition with nucleic acids of the sample, hybridishing the composition of and comparing the complexes with those of a standard, where differences and comparing the composition The sample is from a subject with composition of compounds to differential expression. The sample is from a subject with confidence differential expression with a standard defines an early, mid or late stage of the disease. The composition and or protein encoded by the compounds to identify a ligand which specifically binds a CDNA or protein compounds to identify a ligand which specifically binds a CDNA or protein compounds are selected from DNA, RNA, peptide nucleic acid molecules and compounds are selected from DNA, RNA, peptide nucleic acid molecules and compounds are selected from DNA, RNA, peptide nucleic acid molecules and compounds are selected from DNA, RNA, peptide nucleic acid molecules and compounds are selected from DNA, RNA, peptide nucleic acid molecules and compounds are selected from DNA, RNA, peptide nucleic acid molecules and compounds are selected from DNA, RNA, peptide nucleic acid molecules inhibitors, drug compounds, pharmaceutical agents, transcription factors, repressors, and regulatory proteins. The composition is useful for the diagnosis of prostate cancer. The antibodies are also useful for the diagnosis of disease. This sequence represents a prostate adenocarcinoma cDNA
                                                                                                                                                                                                                                                                          invention describes a composition of a number of human cDNAs that are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melanoma; thyroid tumour; MEL3; MEL7; Thy5; Thy6; Thy11; Thy14; Thy15; rectal cancer; lung cancer; breast cancer; colon cancer; antibody Ki-67;
New composition, useful for treating and diagnosing prostate cancer, comprises human cDNAs that are differentially expressed in prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequence encoding the antigen of monoclonal antibody Ki-67.
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                                                                                                                                                                                  Claim 1; Page 130-135; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA64659 standard; cDNA; 11435 BP
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Wu ID;

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soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
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                                                                                                                                                 New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                          Sequence 11435 BP; 3802 A; 2828 C; 2684 G; 2121 T; 0 U; 0 Other;
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                   Ouyang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ22788 standard; DNA; 11466
                 11-AUG-2003; 2003US-0493546P
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                                                 (GETH ) GENENTECH INC
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                                                                                                                   WPI; 2005-182330/19.
                                                                                   Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                          polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecules for diagnosing and treating melanoma, thyroid tumors, rectal, lung, breast and colon cancers.
                                                                                                                                                                                                                                                                                        old L,
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                                                                                                                                                                                                                                                                                        Scanlan M,
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Matches:
Conservative:
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Bilynsky B;
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                                                                                25-FEB-2000; 2000WO-US004929.
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RODNIN N.
FILONENKO V.
MATSUKA G.
SCANLAN M.
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Query Match:
DB:
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Homo

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic sact sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 11466 BP; 3830 A; 2830 C; 2684 G; 2122 T; 0 U; 0 Other;

00000 Length: Matches: Conservative: Mismatches: Indels: Gaps: 2.53e+039.00 100.0% 100.0% 4.2% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local

(1-11466)US-09-989-890-238 (1-212) x ADQ22788

4052 GCTCTTCTTTCACGCCCCACTTTCCCCA 4026 29 AlaLeuLeuSerArgProLeuSerPro 37 ò

AAZ43872/c ID AAZ43872 standard; DNA; 12493 BP

AAZ43872;

(first entry) 10-MAR-2000

Human cell cycle protein Ki-67 DNA.

Cell cycle protein, Ki-67; therapy; cell proliferation; allergy; tumor treatment; autoimmune disease; scar formation; inflammation; rheumatic disease; transplantation; ds.

Homo sapiens

Location/Qualifiers 197. .9967 /product= "Ki-67" /*tag=

DE19822954-A1

25-NOV-1999

98DE-01022954 22-MAY-1998;

98DE-01022954 22-MAY-1998;

Deinert I; Boehle A, Flad H, Gerdes J,

(BORS-) FORSCHUNGSZENTRUM BORSTEL ZENT MEDIZIN.

2000-039964/04. P-PSDB; AAY50976. Ki-67 gene antisense oligonucleotide.

Disclosure; Page 5-19; 36pp; German.

This invention describes a novel oligoribo- or oligodeoxyribonucleotide, characterized in that, it hybridizes to mRNA that encodes protein Ki-67

The invention relates to a combination comprising a number of cDNAs expressed in prostate cancer. The invention also relates to a method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids by hybridising a substrate with the nucleic acids, thus forming one or more hybridisation complexes, detecting hybridisation complexes, where differences between the standard and the sample complex formation and comparing the complexes formed with standard formation indicate differences between the standard and the sample complex formation also related differential expression of cDNAs in the sample. The differential expression is diagnostic of prostate cancer. The invention also relates to proteins and antibodies related to the CDNAs. at a physiologically acceptable salt concentration. The oligoribo- or oligodeoxyribonuclectide which is complementary to K1-67, a protein active at all stages of the cell cycle except 6 0, is useful for therapy of illnesses with increased cell proliferation and particularly for tractment of tumors, autofmmune diseases, scar formation, inflammation, allergy, rheumatic diseases and defence against transplantation. This sequence encodes the human cell cycle protein Ki-67 which is described in Human; prostate cancer; ss; cDNA combination; differential expression; progression of treatment of prostate cancer. The antibodies are useful New combination comprising cDNAs that are differentially expressed in prostate cancer, useful for diagnosing, treating or monitoring the progression of treatment of prostate cancer. Sequence 12493 BP; 4143 A; 3048 C; 2929 G; 2373 T; 0 U; 0 Other; 12493 9 0 0 0 0 Matches: Conservative: Mismatches: Length: Indels: 5132 GCFCFTFTCACGCCCACTFTCCCCA 5106 US-09-989-890-238 (1-212) x AAZ43872 (1-12493) AlaLeuLeuSerArgProLeuSerPro 37 Gaps: Claim 1; SEQ ID NO 263; 42pp; English. ADE53916 standard; cDNA; 12494 BP Human prostate cancer cDNA #263 29-MAY-2002; 2002US-00252157. 31-MAY-2001; 2001US-0295048P 2.74e+03 9.00 100.0% the method of the invention 29-JAN-2004 (first entry) 4.2% Pearson CI; (PEAR/) PEARSON C I. WPI; 2003-831619/77. Percent Similarity: Best Local Similarity: US2003190640-A1. (FARI/) FARIS M. Homo sapiens. Alignment Scores: 09-OCT-2003. ADE53916; 53 Faris M, Query Match: gene. ADE53916, 888888888888 ò 셤

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Conservative: Mismatches: Indels:

(1-12515)Gaps:

BP.

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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                     Kidney cancer related gene sequence SEQ ID NO:7459.
                                                                                              5132 GCTCTTCTTTCACGCCCACTTTCCCCA 5106
                                                                               29 AlaLeuLeuSerArgProLeuSerPro 37
                                                          US-09-989-890-238 (1-212) x AAA64658
                                                                                                                                                 ABL69122 standard; DNA; 12515
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2000US-0233133P.
2000US-0233617P.
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2000US-0235711P
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25-SEP-2000;
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                                                                                                                                                 The specification describes polynucleotides which are associated with melanoma and thyroid tumors. Specifically, these are MEL3, MEL7, Thy5, Thy1, Thy14, and Thy15. The polynucleotides are useful for diagnosing and treating a patient with melanoma, thyroid tumour, rectal cancer, lung cancer, breast cancer or colon cancer. The present sequence represents a polynucleotide of the invention
  for detecting prostate cancer. This sequence represents a human prostate cancer cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                  Melanoma; thyroid tumour; MELJ; MEL7; Thy5; Thy11; Thy14; Thy15; rectal cancer; lung cancer; breast cancer; colon cancer; antibody Ki-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecules for diagnosing and treating melanoma, thyroid tumors, rectal, lung, breast and colon cancers.
                                                                                                                                                                                                                                                                                                             cDNA sequence encoding the antigen of monoclonal antibody Ki-67.
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                                    Sequence 12494 BP; 4146 A; 3045 C; 2929 G; 2374 T; 0 U; 0 Other;
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Bilynsky B;
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Matches:
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                                                                                                                              Gaps:
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                                                                                                                                                                                                                                           AAA64658 standard; cDNA; 12515 BP.
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RODNIN N.
FILONENKO V.
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SCANLAN M.
OLD L.
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                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (M1) for screening for an antineoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the dara collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, and cancer, infiltrating lobular cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                               Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; gene; human; adipocyte differentiation; obesity; type II diabetes; lipodystrophy; hyperinsulinaemia.
                                                                        Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
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                                                                                                                                                                               Claim 1; SEQ ID NO 7459; 44pp; English.
                                                                       Carter KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD12702 standard; cDNA; 12515 BP.
03-OCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0244867P.
01-NOV-2000; 2000US-0245084P.
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                                                                      Augustus M,
Weaver Z;
                                               (AVAL-) AVALON PHARM.
                                                                                                          WPI; 2002-188264/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score:
Percent Similarity:
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                                                                      PB, ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD12702;
                                                                                   Soppet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
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The invention relates to an isolated cDNA expressed during adipocyte differentiation. The cDNA is useful for treating a subject with a disorder such as obesity, type II diabetes, lipodystrophy or hyperinsulinaemia. The nucleic acid is useful for a high throughput method of using a cDNA to screen several molecules or compounds to identify a ligand which specifically binds the cDNA which involves combining the nucleic acid with several molecules or compounds under conditions to allow specific binding, and detecting specific binding between each cDNA and at least one molecule or compound, thus identifying a ligand that specifically binds to each cDNA. The several molecules or compounds are chosen from DNA molecules, RNA molecules, peptide nucleic acid molecules, mimetics, peptides, transcription factors, repressors and regulatory proteins. The present sequence represents a human cDNA expressed during adipocyte differentiation.
                                                                                                                                                                                             Novel isolated cDNAs expressed in adipocyte differentiation useful for treating subject with disorder such as obesity, type II diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   estrogen receptor-positive invasive breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-989-890-238 (1-212) x ADD12702 (1-12515)
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                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 48; 105pp; English
                                                                                                                                                                                                                                                        lipodystrophy or hyperinsulinemia.
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18-SEP-2002; 2002US-0412049P.
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                                                                                 Schebye XM, Sornasse
                                                                                                                                         WPI; 2003-810888/76.
(SCHE/) SCHEBYE X M.
                             SORNASSE T.
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Best Local Similarity:
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                                                                                                                                                    The invention relates to a method of predicting clinical outcome for a patient diagnosed with cancer by determining the expression level of one or more genes, or their expression products, selected from p53BP2.

cathepsin B, cathepsin L, Ki67/MiBI, and thymidine kinase in a cancer tissue obtained from the patient, normalized against control gene(8), and compared to the amount found in a reference cancer tissue set. The specification also discloses an array comprising polymucleotides hybridizing to the following genes: FOXMI, PRAME, BGL2, STKIS, CEGPI, Ki-ST, GSTH3, PRP, BRG3, NNEI, SURV, GAM13, TFRC, XB-1, DPVD, GSTM3, RPS6KB1, Sro, Chki, IDI, BetRI, p27, CCNBI, XIAP, Chk2, CDC2SB, IGFR, RNESAS, BRCA2, BRCA2, BCRA2, BCRA, BCRA, BCRA, GER, TKI, VDR, CONTISSION, PRINTI, EPHXI, HNF3A, NFKB965, BRCA2, EGFR, TKI, VDR, CONTISSION, PRINTI, EPHXI, IFIA, CDHI, HIFL, IGFRB3, GTSB, Harz and DIABLO, immobilized on a solid surface. The methods are useful for predicting clinical outcome for a
                                   Predicting clinical outcome for a patient diagnosed with cancer comprises determining the expression level of one or more genes, and compared to the amount found in a reference cancer tissue set.
                                                                                                                                                                                                                                                                                                                                                                                                                                            patient diagnosed with cancer, classifying cancer, and predicting the likelihood of long-term survival of a breast cancer patient, or a patient diagnosed with invasive breast cancer or with estrogen receptor (ER)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth, differentiation, blood endothelial cell; BEC; lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGFC-7; VEGF-0; antianglogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      positive invasive breast cancer. This sequence corresponds to a gene sequence whose expression is detected by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
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                                                                                                                Disclosure; SEQ ID NO 313; 198pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-989-890-238 (1-212) x ADG89365 (1-12515)
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WPI; 2003-767536/72
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DB:
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This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the provise that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of composition composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of composition to reactive activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cells, in treating hereditary of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the discorder or in monitoring the efficacy or toxicity of a drug on endothelial cells are endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatical cells that of a human LEC/BEC differentially expressed gene which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the company of the source data given in table if of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
                  Petrova T, Saharinen P, Saharinen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bronchial cancer; cytostatic; tumour-associated protein; cancer detection; metastasis; tumour; gene; ds; human.
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                                                                                                                           Example 1; SEQ ID NO 358; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 AlaLeuLeuSerArgProLeuSerPro 37
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                  Alitalo K, Makinen T,
                                                             WPI; 2003-876899/81.
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                                                                                    P-PSDB; ADN95434
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Wong TW;

Jackson DG,

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Rupnow BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a novel isolated nucleic acid associated with bronchial cancer comprising 489 defined sequences given in the appoint of the invention may be useful for the production of compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and the proteins/peptides encoded by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or classociate for prognosis, detection of metastases and for secondary treatment of the used for prognosis, detection of metastases and for secondary treatment of the unours that have been stabilised or are no longer detectable). Detecting abnormal expression of the DNA sequences provides early diagnosis of bronchial cancers. The present sequence is that of a novel bronchial cancer-associated human gene sequence of the invention.
                                                                                                                                           New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
                                                                           Hermann K, Kinnemann H;
Rosenthal A, Pilarsky C;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
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                                                                           T, Heiden E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
                             (HINZ/) HINZMANN B.
(HERM/) HERMANN K.
(CAST/) HEIDEN CASTANOS-VELEZ
         09-APR-2003; 2003DE-01016701.
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                                                                            Bruemmendorf
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                                                                                                           WPI; 2004-786403/78.
P-PSDB; ADU06545.
                                                                                      Roepcke S,
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Query Match:
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                                                                            Mennerich
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the there a mammal will respond or in responding to an anti-cancer agent that modulates cyclin-dependent kinase (dk) activity. The method comprises measuring the level of one or more blomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed microarrays comprising the biomarkers described, antibodies directed microarrays comprising the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[[5-(1,1-b]methylethyl]-2-caracid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fp. wipo.inft was obtained in electronic format directly from WIPO at fp. wipo.inft the method of the invention.
                                                                                                       Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antityroid; Antidiabetic; Nephrotrorpic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic; Antiallergic; ds; gene; dlagnosis.
                                                                                                                                                                                                                                                                                                                          This invention describes a novel method of predicting or determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                Claim 5; SEQ ID NO 2632; 141pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADY16692 standard; DNA; 12515 BP
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                                                                                                                                            to a cancer treatment comp
dependent kinase activity.
WPI; 2005-163068/17.
P-PSDB; ADX08068.
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                                                                                                                                              Best Local
                                                                                                                                                                                                                                                    RESULT 88
                                                                                                                                                                                                                                                                ADY61174
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                                                                                                                                                                                                                                                                                     immune
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                                                                      New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic; Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic; Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
                                                                                                                                                          an
                                                                                                                                The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating ar related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                         Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
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                              Wu TD;
                             Wood WI,
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                                                                                                                                                                                                                                                               Conservative:
Mismatches:
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                            Ouyang W, Williams MP,
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                                                                                                                                                                                                                                           Length:
Matches:
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                                                                                                                                                                                                                                                                                                                  US-09-989-890-238 (1-212) x ADY16692 (1-12515)
                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                               Claim 1; SEQ ID NO 2498; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2496; 158pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiallergic; ds; gene; diagnosis.
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ID ADY16690 standard; DNA; 12515
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        (GETH ) GENENTECH INC
                                                WPI; 2005-182330/19
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                            Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark H,
                                                                                                                                                                                                                                                                           Best Local Similarity:
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                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                       polypeptide.
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                             Abbas A,
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The invention relates to a method of analyzing differential gene expression associated with breast tumor. The method comprises detecting the over expression or under expression of sequences neighboring the BRB2 (also known as HER2 or Neu) on chromosome 17q12. The polynucleotide expression profiling comprises at least one, preferably at least two, three or all polynucleotide sequences (or its subsequence or complement) selected from predefined polynucleotide sequence sets consisting of: Set 1: SEQ ID NOS: 13.77 (ERBB2), Set 2: SEQ ID NOS: 28-30 (GRB7), Set 3: SEQ ID NOS: 83-85 (MR1D1), Set 4: SEQ ID NOS: 78-80 (GRB74), Set 5: SEQ ID NOS: 41-43 (CDH15), Set 6: SEQ ID NOS: 16, 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression; breast tumor; BRBB2; HBR2; Neu; oncogene; chromosome 17; DNA library; DNA microarray; diagnosis; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analyzing differential gene expression, useful for detecting, diagnosing, staging, monitoring, predicting, preventing or treating breast cancer, comprises detecting an ERBB2 gene expression signature.
The invention relates to an isolated nucleic acid encoding a PRO polypeptide. The polypeptide, agonist or an antagonist, antibody, composition, and method are useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis. The present sequence represents a DNA encoding a PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breast cancer associated human polynucleotide sequence, SEQ ID No:58.
                                                                                                                                                                                                                Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuLeuSerArgProLeuSerPro 37
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27-AUG-2004; 2004US-00928465.
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
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Ginestier C;
                                                                                                                                              polypeptide.
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30-JUN-2005 (first entry)

ADZ09648;

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CC (LTA), Set 7: SEQ ID NOS: 86, 87, 116 (MAPZK6), Set 8: SEQ ID NOS: 54, 55, 11; (PEZMA), Set 21: SEQ ID NOS: 44, 45 (FPRERB), Set 21: SEQ ID NOS: 42, 45 (FPRERB), Set 21: SEQ ID NOS: 48, 45 (FPRERB), Set 21: SEQ ID NOS: 48, 45 (FPRERB), Set 21: SEQ ID NOS: 52, 65, 48, 45 (FPRERB), Set 21: SEQ ID NOS: 52, 65, 48, 45 (FPRER), Set 22: SEQ ID NOS: 56, 59, 41 (FREF), Set 27: SEQ ID NOS: 56, 59, 41 (FREF), SET 29: SEQ ID NOS: 13, 41 (FREF), SET 29: SEQ ID NOS: 13, 415 (FREF), SET 29: SEQ ID NOS: 13, 41 (FREF), SEQ ID NOS: 14, 41 (FREF), SET 29: SEQ ID NOS: 13, 41 (FREF), SET 29: SEQ ID NOS: 14, 41 (FREF), SET 29: SEQ ID NOS: 15, 13 (FREFAIR), SET 13: SEQ ID NOS: 16, 14 (FREFAIR), SET 13: SEQ ID NOS: 19, 10 (FREFAIR), SET 29: SEQ ID 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        slide, glass beads, membranes on glass support or silicon chip. The method of the invention is useful for the identification of an BRBB2 gene expression signature in breast cancer. The methods and sequences are useful for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with breast cancer, and are used to follow up the stage or aggressiveness of a breast cancer. This sequence represents a human polynucleotide sequence located on chromosome
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Sequence 12515 BP; 4166 A; 3048 C; 2928 G; 2373 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
         2.74e+03
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Best Local Similarity:
Alignment Scores:
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DB:
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US-09-989-890-238 (1-212) x ADY61174 (1-12515)

Š g

ADZ09648 standard; DNA; 12515 BP ADZ09648/c ID ADZ096 RESULT 89

cDNA downregulated in senescent cells Incyte ID NO: 412661.2.

27-MAY-2003 (first entry)

ACA03928;

5132 GCTCTTCTTTCACGCCCACTTTCCCCA 5106

ACA03928 standard; cDNA; 12632 BP

RESULT 90

g

29 AlaLeuLeuSerArgProLeuSerPro 37

(1-12515)Gaps:

US-09-989-890-238 (1-212) x ADZ09648

Percent Similarity: Best Local Similarity:

Query Match: DB:

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neoplasm; tumor marker; cytostatic; breast tumor; gene therapy; ds; gene; MK167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for characterizing the state of a meoplastic disease in a subject comprising determining the pattern of expression levels of at least 6, 810,15, 20, 30, 47 or 67 marker genes in a biological sample, comparing the pattern of expression levels with reference patterns of expression levels and characterizing the state of the neoplastic disease in the subject from the outcome of the comparison. The method of the invention demonstrates cytostatic applications and may be useful in characterizing the state of a neoplastic disease in a subject, preferably breast cancer, in gene therapy and for screening for compounds having a curative effect on a neoplastic disease. The current sequence is that of the human breast cancer marker MKIG7 DNA of the invention which is differentially expressed in neoplastic tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Characterizing the state of a neoplastic disease in a subject by comparing the pattern of determined expression levels of marker g a biological sample with reference patterns of expression levels.
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Matches:
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                                                                                     Human breast cancer marker MKI67 DNA.
                                                                                                                                                                                                                                                                              30-JUN-2004; 2004EP-00015374.
                                                                                                                                                                                                                                                                                                             06-OCT-2003; 2003EP-00022587
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P-PSDB; ADZ09813.
REFSEQ; NM_002417.
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                                                                                                                                                                                                           EP1522594-A2
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Tumour-associated antigenic target; TAT; human; overexpression; cancer; tumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; lenkaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;

gene therapy; cytostatic; gene; ss.

29-SEP-2003; 2003WO-US028547. 02-OCT-2002; 2002US-0414971P

WO2004030615-A2. Homo sapiens.

15-APR-2004.

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The invention relates to a combination comprising a plurality of cDNAs, or their complements that are differentially expressed in cancer and cherry proliferative disorders. The combination is useful in detecting changes in expression of genes encoding proteins that are associated with senescence and in diagnosing, staging, treating, or monitoring the progression or treatment of subjects with proliferative diseases such as cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, bone marrow, brain, breast, cervix, colon, oesophagus, gall bladder, bone, ganglia, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid gland, penis, prostate, salivary glands, skin, small intestine, spleen, stomach, testis, thymus, thyroid and uterus. The present sequence represents cDNA of genes that are downregulated in senescent cells
                         adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; teratocarcinoma; adrenal gland cancer; bladder cancer; bone cancer; bone marrow cancer; brain cancer; braest cancer; cervical cancer; colon cancer; heart cancer; liver cancer; lung cancer; muscle cancer; ovarian cancer; kidney cancer; liver cancer; parathyroid gland cancer; postate cancer; parathyroid gland cancer; postate cancer; salivary gland cancer; semall intestine cancer; specie cancer; cance
Human, senescence, ss, gene, cancer, proliferative disorder, leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New combination comprising cDNAs or their complements, useful for detecting changes in expression of genes encoding proteins associated with senescence, and in diagnosing, staging or treating proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12632 BP; 4157 A; 3089 C; 2999 G; 2387 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13; Page 71-76; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                      thyroid cancer; uterine cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002; 2002US-00071766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-FEB-2001; 2001US-0268380P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-328858/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002192678-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHEN/) CHEN H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen H;
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New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or

Zhou Y;

Zhang Z,

Wu TD,

WPI; 2004-347921/32.

(GETH) GENENTECH INC.

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Length:
Matches:
Conservative:
Mismatches:
                                                              Indels:
                                                                                                                                            5270 GCTCTTCTTCACGCCCACTTTCCCCA 5244
                                                                                                     US-09-989-890-238 (1-212) x ACA03928 (1-12632)
                                                                            Gaps:
                                                                                                                               29 AlaLeuLeuSerArgProLeuSerPro 37
                                                                                                                                                                                                127/c
ACN39127 standard; cDNA; 12674
            2.77e+03
                       9.00
100.0%
100.0%
4.2%
                                   Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                                             Query Match:
                                                                                                                                                                                   RESULT 91
                                                                                                                                                                                                ACN39127/
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Tumour-associated antigenic target (TAT) cDNA DNA325386, SEQ ID NO:3074.

(first entry)

18-NOV-2004

ACN39127;

8×4×6×8

BP

the interaction retailers to manning and the properties are oblypoptides, and their related nucleic acids. The TAT polypoptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypoptide polypoptide at least 80% identical to the TAT nucleic acids and polypoptide and polypoptide and polypoptide and antibody specific for a TAT polypoptide; a peptide or organic molecule which binds to a TAT polypoptide; fusion proteins comprising a TAT polypoptide, fusion proteins comprising a TAT polypoptide, fusion proteins comprising a TAT polypoptide, and methods and compositions for the treatment or aliagnosis of cancer in mammals. TAT polypoptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancer, liver cancer, bladder cancer, lung cancer, cervical cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence invention relates to human tumour-associated antigenic target Sequence 12674 BP; 4164 A; 3103 C; 3017 G; 2390 T; 0 U; 0 Other; 00000 Matches: Conservative: Mismatches: chromosome identification and in gene therapy. represents a TAT nucleic acid of the invention Length: Indels: US-09-989-890-238 (1-212) x ACN39127 (1-12674) Claim 1; SEQ ID NO 3074; 7273pp; English. AlaLeuLeuSerArgProLeuSerPro 37 Gaps: .724/c ADF81724 standard; DNA; 12747 BP. 2.77e+03100.0% 100.0% 4.2% prostate cancer or tumor. 9.00 Percent Similarity: Best Local Similarity: Alignment Scores: 29 Query Match: ADF81724/c ID ADF8: RESULT

Dugas M;

us-09-989-890-238.oligo_p2n.rng

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The present invention relates to a method (M1) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prox-1; developmental disorder, Usher Syndrome Type II;
retinal degradation; retinitis pigmentosa.
                                                                                                                                                                                                                                                                                                                                                                    Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12747 BP; 4164 A; 3071 C; 2985 G; 2365 T; 0 U; 162 Other;
                                                                                                                                                                                                                                                                                 Kohlmann A, Schnittger S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2279; 2938pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-989-890-238 (1-212) x ADF81723 (1-12747)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaLeuLeuSerArgProLeuSerPro 37
                                                                                                                                                                (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. (UYLU-) UNIV LUDWIG MAXIMILIANS. (HAFE) HARFRLACH T. (SCHO/) SCHOCH C. (KERN/) KERN W.
                                                                                                                                                                                                                                                                               Haierlach T, Schoch C, Kern W,
Eils R, Brors B, Mergenthaler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 48396 BP
                                                                                     04-NOV-2002; 2002WO-EP012303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2002; 2002US-00162846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2002; 2002US-00162846.
                                                                                                                    05-NOV-2001; 2001EP-00126244
30-APR-2002; 2002EP-00009758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PROX-1 DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG88601 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds; gene; human; ocular disorder;
                WO2003039443-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003224516-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                patient sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-2004
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                                                 15-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 94
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#X#XBXBXXXXXXBX#XXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method (MI) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comparises determining the expression profile of a group of markers in a patient sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kohlmann A, Schnittger S, Dugas M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12747 BP; 4164 A; 3071 C; 2985 G; 2365 T; 0 U; 162 Other;
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9
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 AlaLeuLeuSerArgProLeuSerPro 37
                                                                                                   Cytostatic; Gene therapy; leukaemia; ss
                                                                  Leukaemia-related DNA sequence #2280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukaemia-related DNA sequence #2279
                                                                                                                                                                                                                                                                                                                                       KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Haferlach T, Schoch C, Kern W,
Eils R, Brors B, Mergenthaler S;
                                                                                                                                                                                                                                                                                                                                   DEUT KREBSFORSCHUNGSZENTR
UNIV LUDWIG MAXIMILIANS.
HAFERLACH T.
SCHOOT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF81723/c
ID ADF81723 standard; DNA; 12747
                                                                                                                                                                                                                                                04-NOV-2002; 2002WO-EP012303
                                                                                                                                                                                                                                                                                   05-NOV-2001; 2001EP-00126244
                                                                                                                                                                                                                                                                                                  30-APR-2002; 2002EP-00009758
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                                   (first entry)
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Query Match:
                                                                                                                                                                           WO2003039443-A2
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                                                                                                                                        Unidentified.
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                                 26-PEB-2004
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                                                                                                                                                                                                                                                                                                                                                      (UYLU-) (HAFE/) 1 (SCHO/) 5 (XERN/) 1
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RESULT 93

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variation
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                                                                                                                                                                                                                                                                       276
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                                                                                                                                                                                                                                                                                                     ABS56296
                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                 $86666666666688$$
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                                                                                                                                                                                                                                                                       셤
                                                                                                                                      The invention relates to a compound targeted to a nucleic acid molecule encoding prox-1 and inhibits the expression of prox-1. The compound, composition and methods are useful for treating a disease or condition associated with prox-1, such as a developmental disorder e.g. Usher Syndrome Type II, or an ocular disorder, e.g. retinal degradation or retinitis pigmentosa. They are also useful in research and diagnostics for modulating the expression of prox-1. The present sequence represents a human PROX-1 DNA.
                                                                 New compounds, particularly antisense oligonucleotides targeted to a nucleic acid encoding prox-1 useful for treating a disease or condition associated with prox-1, e.g. cancer, Alzheimer's disease or neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening, diagnosis and therapy of colon tissue for a pathological condition, e.g. colorectal cancer, where elevation of transcription factor Prox-1 expression correlates with a pathological phenotype.
                                                                                                                                                                                                                                 Sequence 48396 BP; 13584 A; 9992 C; 9850 G; 14970 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colorectal tumor; neoplasm; Prox-1; Cytostatic; ds; gene.
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                 (1-48396)
                                                                                                                                                                                                                                                                                                                                                                 CTCCCAAGTTCTCTTGCCTTGCTATCC 101
                                                                                                                     Example 15; SEQ ID NO 11; 99pp; English
                                                                                                                                                                                                                                                                                                                                                      LeuProSerSerLeuAlaLeuLeuSer 32
                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 71; SEQ ID NO 1; 270pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                  US-09-989-890-238 (1-212) x ADG88601
                                                                                                                                                                                                                                                                                                                                                                                                                 ADX70387 standard; DNA; 49275
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9.00
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100.0%
4.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Prox-1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alitalo K, Petrova T,
         (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LICN ) LICENTIA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-152553/16.
P-PSDB; ADX70389.
                                                 WPI; 2004-022080/02
                                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2005014854-A1
                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ADX70387;
                                                                                                                                                                                                                                                                                                                                                      24
                            Dobie KW
                                                                                                                                                                                                                                                                                                      Query Match:
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The invention relates to a method of screening colon tissue for a pathological condition which comprises measuring Prox-1 expression in a biological sample that comprises colon tissue from a mammalian subject, where elevated Prox-1 expression in the colon tissue correlates with a pathological phenotype. The molecule that suppressed expression or activity of Prox-1 is useful in the manufacture of a medicament for the treatment of colorectal cancer. The inhibitor of Prox-1 function in mammalian cells is useful for the manufacture for inhibiting Prox-1 function. The siRNA molecule is useful in the manufacture of a medicament for the treatment of colorectal cancer. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene; de; transporter protein; allelic variant; SNP;
cell proliferation; cell differentiation; cell signalling; antibody;
gene chip; transgenic; therapeutic; diagnostic;
single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                  Sequence 49275 BP; 13857 A; 10175 C; 10034 G; 15209 T; 0 U; 0 Other;
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/standard_name= "Single nucleotide polymorphism"
replace(13656. .13657,TGG)
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-989-890-238 (1-212) x ADX70387 (1-49275)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 LeuProSerSerLeuAlaLeuLeuSer 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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3000. .70546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         name=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace (4249,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human transporter protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace (3962, G)
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/*tag= b
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The invention discloses an isolated human transporter polypeptide, and its allelic variants or orthologues, and the polymucleotides encoding them allelic variants or orthologues, and the polymucleotides encoding concluding cell proliferation, differentiation and signalling processes, including cell proliferation, differentiation and signalling processes, by regulating the flow of molecules, such as ions and macromolecules, into and out of cells. The polymucleotide and polypeptide can be used to raise antibodies, create a gene chip, create a transgenic non-human animal, produce the novel polypeptide, detect the presence of the polypeptide or nucleic acid in a sample, identify a modulator of the polypeptide or nucleic acid in a sample, identify a modulator of the composition, and carrier, that binds to the polypeptide and treat a disease or condition mediated by a human transporter protein which composition, and carrier, that binds to the polypeptide and nucleic acid a patient the composition identified. The peptides and nucleic acid approach or composition in the development of human therapeutics and diagnostic compositions. The peptides are also useful for eliciting an immune response, to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids or as markers for the agents identified are useful for treating transporter-related conditions and a modulator of the peptide is also useful for treating a disorder characterised by an absence of, inappropriate or unwanted expression of the protein gene presented is the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human transporter proteins, useful for developing therapeutic or diagnostic compositions, particularly for developing human therapeutic agents that modulate transporter activity in cells or
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                                                                                                                                         replace(71085,G)
/*tag= ai
/standard_name= "Single nucleotide polymorphism"
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/number= 8 69845, .70296 .**ag= q
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70297. .70543
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ftandard_name= "Single nucleotide polymorphism"
replace(16390,T)
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replace(49419,A)
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ceplace(69067. .69068,AMC)
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/number= 4
replace(15950. .15952,TT)
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15309_.15477
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50697. .53614
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01-JAN-2004

ADC85298;

05-JUN-2003

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The invention relates to recombinant (ADAD1482-ADAD3094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA muclaic acid, a polypeptide (especially an antibody) that specifically binds to the protein, and a biochip comprising CA muclaic acid or fragments thereof. The sequences of the invention were identified using concepenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or a random. Many of these do not carry transduced host oncogenes or direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, includence of acronoma (especially breast cancer, prostate cancer, includence of acronoma or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA mucleic acids, proteins and antibodies are also useful as therespeutic agents and in screening and evaluating drug candidates. The present sequence of the printed page of the printed specification, but was obtained in electronic format directly from WIPPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to recombinant carcinoma associated (CA) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;
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                                                                                                                                                                                                                                                                                                                                              New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1337; 245pp; English.
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                                                                                                                                                                                                                   Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA; secreted; transmembrane; intracellular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinomassociated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
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ID ADC85298 standard; DNA; 96599 BP
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                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morris DW, Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-513603/48.
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Query Match:
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                                                                                                                                                                                                                                                                                          Homo sapiens.
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96600 9 0 0 0

ADA02819;

RESULT 98 ADA02819,

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Pred. No.:

Score:

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New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29168 CTCCCTAGTGCCAGTGCTGCAGCTGGT 29142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: March 17, 2006, 06:24:18
Job time : 793 secs
                                                                                                                                    Claim 1; SEQ ID NO 85; 29pp; English.
                                             Morris DW, Engelhard EK;
           (MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                  WPI; 2004-328562/30
                                                                                                                lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                           New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                         Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;
carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                      60000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine carcinoma associated (CA) nucleic acid #43.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 385; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 LeuProSerAlaSerAlaAlaGly 62
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                                                                                     02-MAR-2001; 2001US-00798586.
23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
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                                                                                                                                                         (SAGR-) SAGRES DISCOVERY
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                      WO2003008583-A2.
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 Mus sp.
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The invention relates to new recombinant nucleic acids. The invention clates to a host cell comprising a recombinant nucleic acid or also relates to a host cell comprising a recombinant nucleic acid. The expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for a bicactive agent capable of binding to a method of screening for a bicactive agent capable of binding to a cartivity of a CAP, a method of evaluating the effect of a candidate a cartivity of a CAP, a method of evaluating the effect of a candidate cartinoma drug, a method of diagnosing carcinoma, a method for inhibiting the activity of a CAP, a method of the activity of a CAP, a method of diagnosing carcinoma, a method of the activity of a CAP, a method of diagnosing carcinoma or propensity to carcinoma Amethod of the activity of a CAP, a method of diagnosing carcinoma or propensity to carcinoma acupacises administering the drug to a patient, removing a carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering the mucleotide sequence. A method of diagnosing carcinoma comprises determining alterations in the expression or activation of a gene comprising the expression of the gene from the patient and comparing the expression of the gene from the patient and comparing the expression of the gene from the first individual and comparing the expression of the gene from the first individual has carcinoma. A method of inhibiting the carcinomas comprises binding an inhibitor to the CAP. The polyaptide specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid are useful for the nucleic acid. The nucleic acid are useful for preparing a composition for diagnosing or treating carcinoma accinome acid of this patent did not form part of the privation specifically privatically prepared as any contactined specification and captined individual and compared specifically because
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;
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22-DEC-2000; 2000US-00747377, 02-MAR-2001; 2001US-00798586

30-NOV-2001; 2001US-00997722

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 Command line parameters:
-MODEL=frame+ p2.n.model -DEV=x1h
-Q=/abss/ABSSWEB_spool/US0998990/runat_16032006_095517_17553/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US0998990/runat_16032006_095517_17553/app_query.fasta_1
-DB=EST -QFWT=fastap -SUTFIX=oligo_p2n.fet -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=coligo -TRANS=human40.cdi -LIST=500
-UNITS=bits -START=1 -END=-1 -MATRIX=0010000000 -MODELOCAL.OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLENE=2000000000 -HOST=abss04
-USER=US09989890 @CGN 1 1 5315 @runat_16032006_095517_17553 -NCFU=6 -ICFU=3
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AA691613 vs16f06.r CB639604 OSJUBEAIIE BH229365 1006151G0 BB123886 BB123886 BB12317 BB752117 BE66459 15225 MA CL173042 104 376 1 B7022859 CM4-MT024 BQ77942 BE708 SQ AA367730 EST78861 CZ647476 OM BA019 BF73165 MAD20910. AA208216 MY23516 CX743742 WM101-3MS AA26411 BST29586 B1722873 CM4-MT024 AA791451 v863321. CT42207 UI-HF-BR0 BF28132 BP828132 BF734813 MR0-KT000 DN175444 NNBO522 CO342580 UMC-PZUM3 BB555423 UI-M-BH4- AV801750 AV801750 AV801750 AV801750	BAJ25301 BJ25301 BJ25301 BJ25301 BJ25301 BJ25301 BJ2521064 OGAMAJ5TC BJ362419 BY362419 CD336356 OV.104412 AJ757959 ELESTER35 BF955895 QV1-NN121 BY613286 BY613286 BZ651071 GGAMAJ5TM AJ125210 MS29£64 X AJ72551 ELESTER22 AV817803 BV613286 BY630962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BY430962 BH2424990 WHE00794 AAJ40018 MG3961 LS AAJ40018 HS 3083 A AG979127 DECORDAIN AG979127 DECORDAIN AAJ25916 BY259166 BY259166 BY259166 AY794074 AV794074 AW123857 UI-M-BH2. BJ25302 BJ25302 BJ25302 BJ25302 BJ25302 BJ25302 BJ25302 BJ25302 BJ25302 BJ25302 AW65657 UI-M-BH2. BJ73168 BY259166 AW794074 AV794074 AW123857 UI-M-BH2. BJ73103 UI-M-BG2- AW602071795 AG2100770 BBF8862 SJ X0260- CC2917795 AG2100770 BBF8862 SJ X0260- CC317795 AG2100770 BBF8863 BB693238 AIG07181 UA-BH4-
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4.2 1022 10 CL468454 9 4.2 1039 9 AQ900370 9 4.2 1072 8 BR037252 9 4.2 1072 8 CF556057 9 4.2 1076 6 CF556057 9 4.2 1084 3 BR455229 9 4.2 1134 10 CL478508 9 4.2 1154 10 CL478508 9 4.2 1154 10 CC4745030 9 4.2 1164 9 CC218420 9 4.2 1164 9 CC218420 9 4.2 1243 3 BR655351 9 4.2 1265 3 BR655351 9 4.2 1265 3 BR655351 9 4.2 1266 3 BR6563307 9 4.2 1266 3 BR6563309 9 4.2 1274 3 BR656000 9 4.2 1266 3 BR656310 9 4.2 1274 3 BR656000 9 4.2 1274 4 CR050000 9 4.2 1274 3 BR656000 9 4.2 1274 4 CR050000 9 4.2 1274 1 AR072000 8 3.8 103 1 DQ050466 9 3.8 125 1 AR072000 8 3.8 125 1 AR072000 8 3.8 125 1 AR072000 8 3.8 125 1 AR072010 8 3.8 125 1 AR08500 8 3.8 155 1 AR08500	DQ045548 1197 bp D Homo sapiens FLJ34633 gene, VIRTUAL genomic survey sequence. DQ045548 DQ045548.1 GI:66896763 GSS. Homo sapiens (human) Homo sapiens (human) Rukaryota; Metazoa; Chordata; Crania Mammalia; Eutheria; Buarchontoglires Hominidae; Homo.
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| organism="Homo sapiens" |
| organism="Rome sapiens" |
| dox zref="taxon:9606" |
| db xref="taxon:9606" |
| clone="IMAGE:6249453" |
| tissue type="ductal carcinoma, cell line" |
| lab_host="DH10B (phage-resistant)" |
| clone lib="NHH MGC_110" |
| clone lib="NHH MGC_110" |
| clone lib="NHH MGC_110" |
| clone lib="crgan: pancreas; Vector: poTB7; Site_1: XhoI; Site_2: BcoRI, cDNA made by oligo-dT priming |
| Site_2: BcoRI, cDNA made by oligo-dT priming |
| Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling And in the laboratory of Gerald M. Rubin (University conficentia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
| Note: this is a NIH_MGC Library."
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AGENCOURT 8341018 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249453
BQ691555
                         147 AGCCCCCACCAAGCCGCCGCACCCGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGC 206
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.

I (bases 1 to 917)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Umpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe.r@mail.nih.gov
Tlasue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CNA Library Arrayed by: The I.M. A.G.B. Consortium (LLML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

High quality sequence stop: 535.

High quality sequence stop: 535.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 AlaCysSerGlyAspProGlyCysGlySerGlyAlaGlyLeuProSerAlaSerAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AlaGly1leAlaSerSerAlaValGluProValCysGlyAspAlaAlaProAlaCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 GCCTGCTCTGGCGACCCTGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCT
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Matches:
Conservative:
Mismatches:
Indels:
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1. 1197
7. Organism="Homo sapiens"
Mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                        (er) PLoS Biol. 3 (6), E170 (2005)
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Alignment Scores: 1.42e-125 Length: 966 Pred. No.: 150.00 Matches: 189 Percent Similarity: 99.0% Conservative: 0 Best Local Similarity: 99.0% Mismatches: 2 Query Match: 2 DB: 2 Gaps: 0 US-09-989-890-238 (1-212) x BE901537 (1-966)	1 SerProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly	Qy 21 GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla 40		Qy 81 LeuArgThrProLeuArgGlyLeuLeuLysProThrGlyProArgSerThrMetGluCys 100 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	121 TrpalaalaSeralaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr	161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg	RESULT 4 AA316608 LOCUS DEFINITION EST188290 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end, mRNA sequence. ACCESSION AA316608 VERSION AA316608. GI:1968936 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ARANISM Homo sapiens (human) ARANISM Homo sapiens (human) ARANISM Homo sapiens (human) ARANISM Homo sapiens (human) ARAMMANISM Homo sapiens (human)	Hominidae; Homo. REFERENCE 1 (bases 1 to 510) AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,
	Db 387 CTGAGGACTCCACTGAGGGACTGCTGAACTGGGCCAACTGGAGGAGCAATGGAGTGC 446 Qy	Qy 121 TrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSerLeuCysIleProThr 140	Qy 141 ArgGlyProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle 160 Db 567 CGAGGCCACCTCCCCAGCCCCTGATGCGAACTCTGCTGCAAGGAGCCATGGCCGATC 626 Qy 161 ProHisProCygAspThrAlaCysProAlaProLeuProValValLeuVal 177 Db 627 CCCTACCTGATGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAGCAACTCTAGCAGCAACTCTAGCAGCAACTCTAGCAACTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCTAGCAACTCAACTCAACTCAACTCAACTCAACTAGCAACTAGCAACTAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACT	SULT 3 901537 CUS CUS FINITION 60 CESSION BE	_	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM842 row: g column: 05 High quality sequence stop: 668. I. 966 Organism="Mono sapiens" Mol_type="mRNA" Mol_type="mRNA" Ab xref="taxon:9606" Clone="IMAGE:3960220" Libh host="DH10B" (phage-resistant)"	/clone_lib="NIH MGC_21" //note=-Organ: placentra; Vector: pOTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCAGNG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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CNZ89134 16-MAY-2004
17000599935935 GRN_PREHEP Homo sapiens CDNA 5', mRNA seguence.
CN289134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae, Homo.

1 (bases 1 to 753)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton L. W.

Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
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from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 rGlySerSerGlnProTrpAlaAlaAlaSerAlaThrProMetLeuSerSerLysAlaSe 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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230 Constitution Drive, Menlo Park, CA 94025, USA
721: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 753 Std Error: 0.00.
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                                                                                                                                                       205 LeuMetCysSerSerSerArgSer 212
                                                                                                                                                                                        422 TTGATGTGCTCATCTTCAAGAAGC 445
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Regenerative Medicine
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KEYWORDS
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ORGANISM
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PUBMED
COMMENT
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AUTHORS
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Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CTGAGGGGACTGCTGAAGCCAACTGGCCAAGGAGCACAATGGAGTGCCCCCCAGCCCTG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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II"
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XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
Tabical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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583 bp mRNA linear EST 17-SEP-2004
BP331524 Sugano cDNA library, rectum Homo sapiens cDNA clone
RCT09504, mRNA sequence.
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1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                              348 GAGTGCCCCCCAGCCCTGATCGTGCACCCCCCAGCCGGCGGATGGCCAGCGGGTTCAAGT
                                                                                                                                                                                                                                                                                                                                                                                       GlnProTrpAlaAlaAlaAlaThrProMetLeuSerSerLysAlaSerLeuCysIle
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                                                                                                                                                                                                                                                                                                       GluCysProProAlaLeuIleValHisProProAlaGlyGlyMetAlaSerGlySerSer
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yauzuki@ins.u-tokyo.ac.jp.
Location/Qualifiers
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'Organism="Homo sapiens"

/mol type="mRNA"

/db_xref="taxon:9606"

/dclone="krc709504"

/rissue type="rectum"

/clone_lib="Sugano cDNA library, rectum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProCysArgAlaGluLysLeuMetCysSerSerSerArgSer 212
                                   1671
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Matches:
Conservative:
Mismatches:
Indels:
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Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Bamil s.wiemannagkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp686B17277) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cggi-bin/products/cl.cgi?CloneID=DKFZp686B17277
Further information about the clone and the sequencing project is
available at http://mips.ggf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="prostate"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MPRPGHPRASGPPRLGPWERPTELCLETYDKPPQPPPSRRTRR
PDPXDPGHPGPESITPEISGSARDALESPTCLLETYPELRGLIKFTGPRSYMECPPALIVH
PPAGGWASGSSQPWAAASATPMLSSKASLCTPTRGPPPQPLWRTPARSHWPIPHPCD
TACPPAPLPVVLVAPRSTILSMSRTWTCRRWAVAPCRAEKLMCSSSRS"
                                                                                                                                                                                                                                                                                                                                                                                                              CK/49558 1671 bp mRNA linear HTC 19-AUG-2004
Homo sapiens mRNA; cDNA DKFZp686B17277 (from clone DKFZp686B17277).
CR749558
                                                               155
                                                                                                   310
                                                                                                                                                                                                                                                                   430
                     250
                                                                                                                                         gSerHisTrpProlleProHisProCysAspThrAlaCysProAlaProLeuProValVa 175
                                                                                                                                                                                                                         175 lLeuValAlaProArgSerThrIleLeuSerMetSerArgThrTrpThrCysArgArgTr 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae, Homo.
I (bases 1 to 1671)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Buarchontoglires, Primates, Catarrhini;
CCTGTGTATCCCTACCCGAGGGCCACCTCCCCCAGGCCCCTGATGCGGACTCCTGCTGCAGG
                                                                                                                                                                    GAGCCACTGGCCGATCCCCCACCCATGCGACACAGCCTGCCCAGCACCTTGCCAGTAGT
                                                                                                                                                                                                                                                    371 CCTCGTGGCTCCGAGGAGTACTATTCTTTCCATGAGTCGGACCTGGACCTGCCGGAGATG
                                                             rLeuCyslleProThrArgGlyProProProGlnProLeuMetArgThrProAlaAlaAr
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                                                                                                                                                                                                                                                                                                       pAlaValAlaProCysArgAlaGluLysLeuMetCysSerSerSerArgSer 212
                                                                                                                                                                                                                                                                                                                                GGCAGTGGCTCCATGTCGAGCCGAGAAATTGATGTGCTCCATCTTCAAGAAGC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="CAH18355.1"
/db_xref="G1:51476785"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
/note="hypothetical protein,
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/organism="Homo sapiens"
/mol_type="mRWA"
/db_xref="taxon:9606"
/clone="DKFZp686B17277"
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1. .1015
| / organism="Homo sapiens" |
| / nol_type="mRNA" |
| / nol_type="mRNA" |
| / db xref="taxon:960" |
| / clone="IMAGE:3947861" |
| / tab ube type="adenocarcinoma cell line" |
| / tab host="DH10B" (phage-resistant) |
| / clone lib="NIH MGC_9" |
| / clone lib="NIH MGC_9" |
| / note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-df priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB741035 1015 bp mRNA linear EST 15-SEP-2000 601594018F1 NIH MGC_9 Homo sapiens cDNA clone IMAGE:3947861 5', mRNA sequence.
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I (bases 1 to 1015)

S NIH-MGC http://mgc.ncd.nih.gov/.

Inth-MGC http://mgc.ncd.nih.gov/.

Inth-MGC http://mgc.ncd.nih.gov/.

Inth-MGC http://mgc.ncd.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTD

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM810 row: d column: 06

High quality sequence stop: 752.
                                                                                                                                                                                                                                                                                                                                                                                     161 ProHisProCysAspThrAlaCysProAlaProLeuProValValLeuValAlaProArg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 CGAGGGCCACCTCCCCAGCCCCTGATGCGGACTCCTGCTGCAAGGAGCCACTGGCCGATC 125
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                             141 ArgGlyProProGlnProLeuMetArgThrProAlaAlaArgSerHisTrpProIle
                                                                                                                                                                                                                                                               6 TGGGCAGCAGCTTCAGCTACCCCGATGTTAAGCTCAAAGGCATCCCTGTGTATCCCTACC
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Mismatches:
Indels:
/note="mammary gland tumor"
                                                                     Length:
Matches:
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Best Local Similarity:
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1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Sugano cDNA library, mammary gland OCUB-F"
                                                                                                                                                                                                                                                                                                                                               147 CAGAGAGCATTACCTTCTCTGGCTCTGCTGAGCCGGCCCTTGAGTCCCCCACCTGCT
                                                                                                                                                                                               1 SerProHisGlnAlaAlaAlaProValAspGlnThrProArgThrLeuAlaThrMetGly
                                                                                                                                                                                                                                                                        21 GlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgProLeuSerProProAla
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shizrokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@img.u-tokyo.ac.jp.
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0 0
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                              Length:
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Conservative:
Mismatches:
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/db xref="taxon:9606"
/clone="OFR07979"
/tissue type="mammary gland"
/cell_line="OCUB-F"
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1. .582
/organism="Homo sapiens"
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BP315176.1 GI:52244151
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Homo sapiens
                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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               Alignment Scores:
Pred. No.:
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/organism="Homo sapiens"
/mol_type="maxkA"
/db_xref="taxon:9606"
/dev_steage="Adult"
/clone_lib="HT0454"
/note="forgan: head_neck; Vector: puc18; Site_l: Smal;
/note="forgan: head_neck; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Garived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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601299865F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629848 5',
                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM1-HT0454-170
100-003-f07&t3=2000-01-17&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 244.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                      expressed
 de Souza, S.J.
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                 Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF sequence tags
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F.,
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1 (bases 1 to 244)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE162756 244 bp mRNA linear EST 21-JUN-2000 PMI-FT0454-170100-003-£07 HT0454 Homo Bapiens CDNA, mRNA sequence. BE162756.1 GI:8625477
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insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDMA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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//db _tref="texton:9606"
//clone="InkGE:3629848"
//tissue_type="choriocarcinoma"
//lab host="Bh108 (phage-resistant)"
//clone lib="NIH MGC 21"
//clone 
                  Hominidae; Homo.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIAL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at: image.llnl.gov
Plate: LicM317 row: a column: 17
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Pan troglodytes FLJ34633 gene, VIRTUAL TRANSCRIPT, partial
sequence, genomic survey sequence.
DQ045549.1 GI:66896764
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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84
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Matches:
Conservative:
Mismatches:
Indels:
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High quality sequence stop: 482.
Location/Qualifiers
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58.00
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Best Local Similarity:
Query Match:
DB:
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                                           REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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DQ045549
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VERSION
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BE741110 623 bp mRNA linear EST 15-SEP-2000 601593919F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947885 5',
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Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Whibiaz,M.J., Rledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
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I (bases 1 to 1181)

Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,

Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,

Mitce,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

A Scan for Positively Selected Genes in the Genomes of Humans and

Chimpanzees
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                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, cocyvile, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 AGCCCCCACCAAGCGGCGCACCGGTAGACCAGACCCCAAGGACCCTGGCCACCATGGGC
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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51
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AlaCysSerGlyAspProGlyCysGlySerGly 51
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Matches:
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GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
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/gene="FLJ34633"
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BE741110.1 GI:10155102
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Homo sapiens cDNA clone IMAGE:5502726
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: image.lln!oy/image/html/iresources.shtml Seq primer: -40FP from Gibco High quality sequence stop: 112.
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Inchange I to 975)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Contact: Robert Strau
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/db_xref="taxon:9606"
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5', mRNA sequence.
EM460277
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Best Local Similarity:
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TITLE
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BM460277
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone='IMAGB: 1947885"
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/clone lib='Organ: ovary; Vector: poTB7; Site 1: XhoI; Site 2:
/clone lib='NHIM Mac 9"
/clone lib='Organ: ovary; Vector: priming. Directionally
/clone libe made by oligo-dr priming sin
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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bb14f07.yl NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2962885 5',
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
Plate: LLCWBIO row: e column: 06
High quality sequence stop: 615.
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1 (bases, Homo.)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Paparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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            Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
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AW732798.1 GI:7633136
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/organism="Pongo pygmaeus"
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1. (Dases 1 to 277)

2. Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

2.1C Frontier Korean EST Project 2001

L. Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

S. Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4409
                                                         /organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="taxon:9606"
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Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z77 bp mRNA linear EST 04-APR-2002
K-EST0026481 S9SNU601 Homo sapiens cDNA clone S9SNU601-20-C05 5',
BQ081980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 ProAlaProLeuProValValLeuValAlaProArgSerThrIleLeuSerMetSerArg 188
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Mismatches:
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Plate: 20 row: C column: 05
High quality sequence stop: 277.
Location/Qualifiers
Plate: LLAM12141 row: f column
High quality sequence stop: 659.
Location/Qualifiers
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Homo sapiens
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20.8$
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Best Local Similarity:
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BQ081980
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AUTHORS
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/call_type="Spithelial"
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/call_line="Sbithelial"
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Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with batceraia lalkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sfis site by treatment of TA RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfis oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into Drail! - digested pME185-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coll Toplof* by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
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DKFZp469G0138_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469G0138_5', mRNA sequence.
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This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Bmail s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 ACCCTGGCCACCATGGGCCCAGAGAGCATTACCTTCATCTCTTGCTCTGCTGAGCCGGCCC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 ThrLeuAlaThrMetGlyGlnArgAlaLeuProSerSerLeuAlaLeuLeuSerArgPro 34
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Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
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Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 276)
Ansorge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
Mewes, H. W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pongo pygmaeus mRNA (Ansorge, W., Krieger, S., Regiert, T., et al.)
Unpublished (2004)
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Matches:
Conservative:
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CR763815.1 GI:52602277
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/tlssue type="choriocarcino"
/clone=lib="NHH MGC_21"
/noce="Crgan: placenta; Vector: pOTB7; Site_1: XhoI;
/noce="Crgan: placenta; Vector: poTB7; Site_1: NhoI;
/noce="Crgan: placenta; Vector: poTB7; NhoI; NhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG335647 101H_MGC_21 Homo sapiens cDNA clone IMAGE:4541898 5',
/mol_type="mRNA"

/db Xref="texxon:9600"

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/tissuc_type="kidney"

/dev stage="adult"

/lab_nost="DH108"

/clone lib="469 (synonym: pkid1)"

/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.

I (bases 1 to 928)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

Plate: LLCM1221 row: c column: 19

High quality sequence stop: 496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                              276
                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-989-890-238 (1-212) x CR763815 (1-276)
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BG335647.1 GI:13142085
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20.00
100.0%
100.0%
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               9.48
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
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BG335647
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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928

Length:

1.6e-06

Alignment Scores: Pred. No.:

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BG335025
BG335025.1 GI:13141463
EST.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Mismatches:
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Homo sapiens
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Final: 1. LewinGuluc.edu

Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack, Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Soares normalized bovine placenta"
/note="Organ: placenta; Vector: pT773Pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 485)
Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson, J.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR PRIMETE
PCR PRIMETE
FORWARD: TAATAACGACTCACTAAAGG
BACKWARD: ATTAACCCTCACTAAAG
INSERT EBP250025B20 row: B column: 12
Seg primer: AGCCGATAACAATTCACACAGGA
High quality sequence stop: 485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 .485
/organism="Bos taurus"
/mol_type="mRNA"
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/clone="BP250025B20B12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female"
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100.0%
5.7%
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Unpublished (2000)
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12.00
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Fax: 217 244 5617
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                          51801, USA
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/mol_type="mtWA"
/strain="mtx FVB/N, CS7BL/6J"
/db xref="taxon:10090"
/clone="IMAGB:366690"
/tisbue_type="tumor, gross tissue"
/dev stage="7" months"
/lab_host="DH10B"
/clone lib="NOI CGAP Mam5"
/clone lib="NOI CGAP Mam5"
/note="organ mammarx"
/sice 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                                                                                                                                                                                       Outbulse inter.

Outbulse (1997)

Other ESTs: uy88210.x1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                       BF150866 425 bp mRNA linear EST 29-DEC-2000 uy88910.yl NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:366690 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 10-OCT-2000
                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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BP250025B20B12 Soares normalized bovine placenta Bos taurus CDNA
clone BP250025B20B12 5', mRNA sequence.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: -40RP from Gibco
High quality sequence stop: 395.
Location/Qualifiers
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                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                          BF150866
BF150866.1 GI:11032261
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BF041373.1 GI:10758428
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Bos taurus (cow)
                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:1427458
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Best Local Similarity:
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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BF041373
                                                                                                          ACCESSION
RESULT 20
                    BF150866
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BES33148 609 bp mRNA linear EST 09-AUG-2000 601235445F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3599314 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                             269 AGCCCCCCCCCTGCTGCTCTGGCGACCCTGGG 304
                                                                                                                                                                                     47
                                                                                                                                                                                   36 SerProProPlaAlaCysSerGlyAspProGly
Length:
Matches:
                                                                                                                                             US-09-989-890-238 (1-212) x BF041373 (1-485)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                            BE533148.1 GI:9761793
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Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pescole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Ogi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, W.S., Setou, M., Shimada, K., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watunabe, Y., Wang, L., Yang, Z., Zavolan, M., Zhu, Y., Yangsawa, M., Yang, I., Yang, L., Yang, Z., Zavolan, M., Zhu, Y., Zamer, A., Carninci, P., Hayatsu, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itch, M., Xagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 679-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEM integrated sequence analysis (RRSA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itob,W., Kagawa,I., Kwai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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/clone_lib="RIKEN full-length enriched, adult inner ear"
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Mismatches:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Glires; Rodentia;

Sciurognathi; Murcidea; Muridae; Murinae; Mus.

1 (bases 1 to 657)

S (kazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schrimi, L.M., Kanapin, A., Matsua, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A.,

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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               657 bp mRNA linear EST 17-DEC-2002 BY753126 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930111008 5', mRNA sequence.
                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.G.E. Consortium/LiNL at:
http://image.lln.gov
Plate: LiAM8781 row: i column: 11
High quality sequence stop: 587.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes="Organ: mammary; Vector: pcWV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
         1 (bases 1 to 609)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mismatches:
Indels:
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clone="IMAGE:3599314"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                  Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Sciurognathi; Murcidae; Muridae; Musinae; Mus.

Sciurognathi; Murcidae; Muridae; Musinae; Mus.

Sciurognathi; Murcidae; Muridae; Mus.

S NIH-MagC http://mgc.nd.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LONDablished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

Contact Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

Http://image.llnl.gov

Londation/Qualifiers

Location/Qualifiers

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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroldea, Muridae, Murinae, Mus.
    602903535F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5033097
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Conservative:
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/organism="Mus musculus"
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                                                                    BI156000.1 GI:14616001
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Query Match:
DB:
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AUTHORS
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/note="Organ: mammary; vector: pCMV-SPORT6; Site 2: NotI; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1866 row: g column: 06
High quality sequence stop: 676.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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                                                                US-09-989-890-238 (1-212) x BY753126 (1-657)
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Mus musculus
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BI156000
LOCUS
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BI653517
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BI159562 746 bp mRNA linear EST 05-JUL-2001 602919525F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5059854 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="NIC CGAP Mam2"
//note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall;
//note="Organ: pcomparation color: pcomparat
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Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LiAM1162 row: a column: 07

High quality sequence start: 3

High quality sequence start: 3

High quality sequence start: 3
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov.m column: 03 Plate: LLAM11044 row: m column: 03
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/dev_stage="5 months"
/lab_host="DH10B"
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/strain="129,C57BL/6J,FVB/N"
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                                                                                                                   High quality sequence stop: 735
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/clone="IMAGE:5005226"
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/clone="IMAGE:5059854"
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/strain="FVB/N-3"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires;

Sciurognathi; Murcidae; Muridae; Murinae; Mus.

B 1 (bases 1 to 738)

S NIH-MGC http://mgc.nci.nih.gov/.

I (npublished (1999)

L (ontact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

COND Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Tray Dry The I.M.A.G.E.

CDNA Library Tray Dry The I.M.A.G.E.

CDNA Library Tray Dry The I.M.A.G.E.

DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1284 row: e column: 05
High quality sequence stop: 720.

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S02873115T NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5005226 5',
   National Institutes of Health, Mammalian Gene Collection (MGC)
                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
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/mol_type="mRNA"
/strain="Czech II"
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went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: InCYLCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: LLAMIGA2 row: o column: 20
High quality sequence start:
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                        B1905713 746 bp mRNA linear EST 16-OCT-2001 03166180F1 NCI_CGAP_Lu33 Mus musculus,cDNA clone IMAGE:5254507 5',
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
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Pred. No.:
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BI905713
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DGB/1324 1NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4923597 5', mRNA sequence.
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/clone="thkdE:4923597"
/clone="thkdE:4923597"
/lab_host="DH10B Hage-resistant)"
/clone lib="NCI CGAP SG2"
/note="Organ: salivary gland; Vector: pCNV-SPORT6; Site 1:
Not!; Site_2: Sali, Cloned unidirectionally. Primer: OlTgo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.

Tissue Procurement: Jeffrey B. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiML at:

http://image.llnl.gov
Plate: LiAMM10845 row: c column: 22

High quality sequence start: 114

High quality sequence stop: 750.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                Gaps:
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Mus musculus
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1 (bases 1 to 1040)

1 (bases 1 to 1040)

1 (bases 1 to 1040)

2 NIH-MGC http://mgc.nci.nih.gov/.

2 National Institutes of Health, Mammalian Gene Collection (MGC)

3 National Institutes of Health, Mammalian Gene Collection (MGC)

4 Unpublished (1999)

5 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: Gilbert Smith, Ph.D.

5 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

8 Bonaldo, Ph.D.

5 CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

5 DNA Sequencing by: Incyte Genomics, Inc.

6 CDNA Library Arrayed by: Consortium/LLNL at:

7 CDNA Library Arrayed by: Consortium/LLNL at:

8 Http://mage.llnl.gov

8 Http://mage.llnl.gov

8 High quality sequence start: 29

8 High quality sequence stop: 909.

8 High quality sequence stop: 909.

8 High quality sequence stop: 909.

9 Norganism=-mans musculus"

1 Nordanism=-mans musculus"
                                                                                      Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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RPCI-11-177D15.TJ RPCI-11 Homo Bapiens genomic clone RPCI-11-177D15, genomic survey sequence.
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                                                                   Mus musculus (house mouse)
                                 BI411303.1 GI:15172226
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                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llhl.gov
Plate: LLAM11645 row: p column: 03

High quality sequence start: 68

High quality sequence stop: 927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI411303
LOCUS BI411303 14-AUG-2001
DEFINITION 602964692F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5119942 5',
                                                                        bl905189 944 bp mRNA linear EST 16-OCT-2001
603167516F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5255666 5',
mRNA sequence.
                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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333 GGGCTGCCTTCTGCTTCCGCCGCTGCAGGCATTGCC 368
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/organism="Mus musculus"
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/strain="Czech II"
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                                                     RESULT 31
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GSS 23-MAR-1999

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Length:
Matches:
Conservative:
Mismatches:

Indels:

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Homo sapiens
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                                                                                                                                                                   AL Unpublished (1997)
Cher GSSS: RPCI-11-177D15.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 304 838 0200
Fax: 304 Bar 0200
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Fax: 305 Fax: 306 Far 0200
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Mammalia; Butheria; Buarchontóglires; Primates; Catarrhini;
                                1 (bases 1 to 328)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
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1 (bases 1 to 257)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone lib="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
fammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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/db_xref="GDB:7567670"
/db_xref="taxon:9606"
/clone="RPCI-11-177D15"
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BF115064
BF115064.1 GI:10984540
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Class: BAC ends
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: 40UP from Gibco
High quality sequence stop: 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NCI CGAP Kidl1"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco R1; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and se circles were made in vitro. PolTowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 150552-1502855). Subtraction by Bento Soares and M. Patina Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strauaberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R..
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.,
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 277)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3134161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="DH10B"
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Unpublished (1997)
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Length:
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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'clone="IMAGE:3259655"
                                                                                                                                                                                                                                                 Fatima Bonaldo.
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Homo sapiens
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/lab_host="DH10B"
/clone="LD="NCI CGAP Kidl1"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco R1;
Plasmid DNA from the normalized library NoT CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clonelDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R..

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R..

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.

Location/Qualifiers
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296 bp mRNA linear EST 12-DEC-2000
naa48hl2.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:3259655 3'
similar to SW:FKHR_HŪMAN Q12778 FORK HEAD DOMAIN PROTEIN FKHR. [1]
;, mRNA sequence.
BF590030.1 GI:11682354
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (Dases 1 to 296)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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110
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Matches:
Conservative:
Mismatches:
Indels:
                 Trace considered overall poor quality
Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Homo sapiens
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/organism="Homo sapiens"
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//wol_type="mRNA"
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/clone_lib="MCT_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco R1;
Plasmid DNA from the normalized library NoT_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500522-15028855). Subtraction by Bentc Soares and M.
Fatima Bonaldo.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 2004)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 796 Std Error: 0.00
Seg primer: -400P from Glaco
High quality sequence stop: 248.
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Mismatches:
Indels:
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ORIGIN

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Best Local Similarity:
Query Match:
DB:
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KEYWORDS
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Sciurografian; Murciace; Murlace; Murlace; Mus.

Nikaido,T., Osato,N., Saito,R.; Suzuki,H.; Yamanaka,I.;

Kiyosawa,H., Yagi,K., Tomaru,Y.; Hasegawa,Y., Nogami,A.;

Kiyosawa,H., Yagi,K., Tomaru,Y.; Hasegawa,Y., Nogami,A.;

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J.; Schriml,L.M.; Kanapin,A.;

Rischer,C.F., Forrest, K.W.; Blake,J.A.; Bradt,D.; Brusic,V.;

Batalov,S.; Beisel,K., Frazer,K.S., Dalla,E., Dragani,T.A.;

Fletcher,C.F., Forrest, M.; Frazer,K.S., Dalla,E., Dragani,T.A.;

Fletcher,C.F., Korrest,A.; Frazer,K.S., Dalla,E., Dragani,T.A.;

Gariboldi,M.; Gissi,C.; Godik,A.; Gaugh,J.; Grimmond,S.;

Kawaji,H.; Kawasawa,Y.; Kedzierski,R.M.; King,B.L.; Konagaya,A.;

Kurochkin,I.V., Lee,Y.; Lenhard,B.L.; Konagaya,A.;

Kurochkin,I.V., Lee,Y.; Lenhard,B.L.; Miki,H.; Nagashima,T.;

Numata,K., Oxido,T.; Pavan,W.J.; Pertea,G.; Pescole,G.;

Petrovsky,N.; Pillai,R.; Ponttius,Ju. Qi., Ci.), Ramachandran,S.;

Ravasi,T.; Reed,J.C.; Reed,D.J.; Reid,J.; Ring,B.Z.; Ringwald,M.;

Sandellin,A.; Schneider,C.; Semple,C.A.; Setou,M.; Shinada,M.; Yang,L.; Yuan,Z.; Zavolan,M.; Shinak,T.; Kawai,J.; Natawa,T.; Fukuda,S.; Hara,A., Hashizume,W.; Inotani,R.; Jahi,Y.; Arakawa,T.; Fukuda,S.; Hara,A., Hashizume,W.; Inotani,R.; Jahi,Y.; Kanaya,J.; Arakawa,T.; Fukuda,S.; Hara,A., Hashizume,W.; Inotani,R.; Jahi,Y.; Rogers,J., Birney,B. and Hayashizahi,Y.; Sasaski,D.; Shizak,K.; Arakaya,J.; Shizak,K.; Araka,J.; Sakazume,M.; Shizak,Y.; Arakawa,T.; Pukuda,S.; Hara,A., Hashizume,W.; Malsawa,R.; Shizak,Y.; Sasaski,D.; Shizak,Y.; Arakawa,J.; Shizak,Y.; Sasaski,D.; Shizak,Y.; Shiza
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The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-85-803-922
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY130650 RIKEN full-length enriched, adult male brain Mus musculus 88730650 RIKEN full-length enriched, adult male brain Mus musculus cDNA clone L630092H16 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukāryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carnind:p., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itch,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Buarchontoglires; Glires; F
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
Mus musculus
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Query Match:
                                                                                                                                                                                                      Percent Similarity:
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BY130650/c
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PUBMED
COMMENT
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TITLE

VERSION KEYWORDS SOURCE

LOCUS

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Ohno, M., Sakai, K., Sakazume, N., Sagaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Shull-Length Mouse CDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper seelected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

NIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence Clustering for construction of a norredundant cDNA library was prepared and sequenced in Mouse Genome CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genome CStences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL973065
AL973065 XGC-gastrula Xenopus tropicalis cDNA clone TGas121p21 5', mRNA sequence.
AL973065 GI:25796660
EST.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 AlaGlyLeuProSerAlaSerAlaAlaAla 61
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    .312
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="male"
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Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Raid, J., Ring, B. E., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shingwald, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wanner, L., Wahlestedt, C., Wang, Y., Watenabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatun, N., Birozane Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibaca, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contract: Yoshinge Hayabilizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tgurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-reseggec.riken.jp, URL:http://genome.ggc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakarume,N., Saasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequence Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
norredundant cDNA library. Genome Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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    .325
    /organism="Mus musculus"

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/clone="L630036B03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.

1 (bases 1 to 325)
S (bazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaldo,I., Osatoo,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.B., Cousins,S., Dalla,B., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY125377 RIKEN full-length enriched, adult male brain Mus musculus CDNA clone L630036B03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="gastrula" (stages 10.5-12 mixed)" |
|/lab_host="Escherichia coli XL1-blue" |
|/clone lib="XGG-gastrula" |
|/note="Vector: pCS10"; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS10" with EcoRI at the 5' end and NotI at the 3' end."
                                             Xenopus tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura; Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Silurana.
1 (bases 1 to 322)
1 Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                  Hinxton, Cambridgeshire, CB10 1SA, UK
Emal: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
YROPTCALIS SEQUENCE 1D: TGas121p21.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Astron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322
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Mismatches:
                      Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 322
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="TGas121p21"
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Mus musculus
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Best Local Similarity:
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DB:
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ORGANISM
                                                    ORGANISM
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JOURNAL
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AUTHORS
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BP423898 Homo sapiens small intestine Homo sapiens cDNA clone HIE07478r 3', mRNA sequence.
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/tissue type="small intestine"
/clone_lib="Homo sapiens small intestine"
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Location/Qualifiers
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/db_xref="taxon:9606"
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PUSISOR NAME AND ADDRESS RIKER Fill-length enriched, whole jointe Mus musculus CDNA close 1200004811 5', mRNA sequence. The control of the co
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Contact: Yoshihide Hayashizaki
     Nature 420, 563-573 (2002)
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyoswa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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Chothia,C., Corbani,L.E., Cousins,S., Dagani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaagterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustinoich,S., Hirokawa,N., Jackson,I.J., Maryls,B.D., Konagaya,A.,
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Maltais,L., Marchionni,L., McKenste,D., Mki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petroveky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY338512 11-DEC-2002
BY338512 RIKEN full-length enriched, whole joints Mus musculus cDNA
clone L230015C04 5', mRNA sequence.
Tissues were provided by Vassilis Aidinis (Blomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                           /tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L230004B21"
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Fax: 81-45-50.9216

Email: genome-resognscriken.jp, URL:http://genome.gac.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishli, Y., Itoh, M., Kawai, J., Konno, H.,
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Encyclopedia Project of Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 11-DEC-2002
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare mouse tissues.
Tissues were provided by Vassilis Aidinis (Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/clone_lib="RIKEN full-length enriched, whole joints"
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/strain="C57BL/6J" /db_xref="taxon:10090" /clone="1320021G07"

us-09-989-890-238.oligo_p2n.rst

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Alignment Scores:
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                                                                                                 Okazaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kayosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, H., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, H., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K.W., Blake, J.A., Brusic, V., Chothia, C., Corbani, L.B., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Razer, K.S., Gaasterland, T., Garibodid, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Lehard, B., Lyons, P.E., Marlet, E.D., Kanaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lechard, B., Lyons, P.B., Maltais, E.D., Kanai, A., Marchioni, L., Mackenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertee, G., Pesole, G., Petrovsky, N., Pillai, K., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Serul, M., Schumer, A., Yang, L., Wanger, L., Wahlested, C., Wang, Y., Watanabe, Y., Wallaing, L.G., Wahlested, C., Wang, Y., Watanabe, Y., Wallaing, L.G., Wahlaw-Boris, A., Yanagisawa, M., Yang, L., Mayazaki, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Wanki, K., Kawai, J., Aizawa, K., Shirakwa, T., Konno, H., Nakamura, M., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y., Materston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60, 770 full-length cDNas
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Fax: 81-45-503-9226

Eaxi: 81-45-503-9226

Exai: 81-45-503-9226

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Exai: 81-45-503-9226

Aizawa, K., Akimura, T., Carninci, P., Fukuda, S., Aizawa, Y., Indonara, E., Nunazaxi, E., Munazaxi, T., Nunazaxi, T., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shizaxi, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Pull-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library was prepared and sequenced in Mouse Genome Encyclopedia real-time sequence Science Laboratory in Riken Genome Construction of Encyclopedia Project of Genome Exploration Research Group in Riken Daivision of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.
Tissues were provided by Takashi Ishikawa ( Department of Surgery
Tissues were provided by Takashi Ishikawa ( Department of Surgery
2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama
236-0004 Japan ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
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/organism="Mus musculus"

source

PEATURES

/mol_type="mRNA"

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CD598944 153 Zebrafish Kidney Marrow CDNA library Danio rerio CDNA
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/clone lib="zebrafish Kidney Marrow cDNA library"
/clone lib="zebrafish Kidney Warrow cDNA library"
/note="Organ: kidney; Vector: pBS-CMV; Site_1: Xho!;
Site_2: ECORI; Total RNA was extracted from the kidney
tissues of mature zebrafish. The poly (A)+ RNA fraction
was separated from total RNA by oligo (dT) callulose
chromatography. Library was initially constructed in the
lambdaZAP Express vector (Stratagene) and in vivo excised
into pBS-CMV vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Song, H.D., Sun, X.J., Deng, M., Zhang, G.W., Zhou, Y., Wu, X.Y., Sheng, Y., Chen, Y., Chen, Y., Ruan, Z., Jiang, C.L., Pan, H.Y., Zon, L.I., Kanki, J.P., Liu, T.X., Look, A.T. and Chen, Z. Hematopoietic gene expression profile in zebrafish kidney marrow Proc. Natl. Acad. Sci. U.S.A. 101 (46), 16240-16245 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Chen Z.
State Key Lab for Medical Genomics
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University
/cell type="stroma cell"
/clone_lib="RIKEN full-length enriched, stroma cell"
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Matches:
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                                                                                                                                                                                                                                                                                                             52 AlaGlyLeuProSerAlaSerAlaAla 61
                                                                                                            Length:
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 86-21-64740490
Fax: 86-21-64743206
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Best Local Similarity:
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Mus musculus
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Sclurogatani, mutoloce; mutinae; mus.

Nikaidoni, osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaidoni, O., Osato, M., Saito, R., Suzuki, H., Yangami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quascerbush, J., Schriml, D., Brusic, V., Chothia, C., Corbani, L. B., Cousins, S., Dalla, E., Dragani, T. A., Pletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T. A., Gustincich, S., Hirokawa, N., Yackson, J. J., Jarvis, B.D., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Majott, D.R., Maltais, L., Marchiconni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Pescole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandan, S., Ravasi, T., Reed, J.C., Red, J.W., King, B.Z., Ringwald, M., Sundelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sungia, T., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wang, T., Yang, L., Hayatu, N., Hirozane-Kishikawa, T., Yanki, K., Kawai, J., Aizawa, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, J., Mirney, B. and Hayashizaki, Y., Rogersho, Rogersho, M., Sato, K., Shiraki, Y., Sabaki, W., Sasaki, D., Shibata, K., Shinayais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNA
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Email: genome-resegec.riken.jp, URL:http://genome.gsc.riken.jp/

Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,

Aizawa,K., Akimura,T., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,

Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,

Ohno,M., Sakai,K., Sakai,W., Wati,K., Watahiki,A., Muramatsu,M. and

Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subrraction of cap-trapper-selected CDNAs to

prepare full-length CDNa libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                      27 SerLeuAlaLeuLeuSerArgProLeuSer 36
                                                              US-09-989-890-238 (1-212) x CD598944 (1-350)
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BY343852/c
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Mus musculus Butheria; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognachi; Murcidae; Murinae; Mus.

1 (bases 1 to 355)

2 (Azaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yadi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Rume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Batalov, S., Batalo, V., Brade, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I. J., Jarvis, B. D., Kanai, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasai, T., Reed, J. C., Reed, J. C., Semple, C., Setcu, M., Shinada, K., Sundellin, A., Schneider, C., Setcu, M., Stanabe, Y., Sultana, R., Nagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Sultana, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Tissues were provided by Vassilis Aidinis (Bnomology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                      Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="whole joints"
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Location/Qualifiers
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PUBMED COMMENT

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wbolcos. INCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2304398 3' elimilar to SW:FKHR_HUMAN Q12778 FORK HEAD DOMAIN PROTEIN FKHR. [1] ;, mRNA sequence.
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BF733006
BF733006.1 GI:12058081
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Itsus Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can b
                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                             1 (bases 1 to 362)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Seq primer: -40UP from Gibco
High quality sequence stop: 349.
Location/Qualifiers
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-resegec.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequence din Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Brivsino of Experimental Animal Research in Riken contributed to
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Haydeutu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shino, M., Waterston, R., Lander, B.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analyais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
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further details.
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FEATURES

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Nkaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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Itoh,M., Kagawa,I., Miyazaki,A., Sasaki,D., Shibaca,K.,
Shinagawa,A., Yasunishi,A., Sakai,K., Sasaki,D., Shibaca,K.,
Shinagawa,A., Yasunishi,A., Soshino,M., Waterston,R., Lander,E.S.,
Analysis of the mouse transcriptome based on functional annotation
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

Sciences Center(GSC), Yokohama Institute
The Institute of E Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tgurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216

Email: 81-45-503-9216

Email: genome-reseggsc.riken.jp, URL:http://genome.gsc.riken.jp/
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Ohno,M., Sakai,K., Sakaumira,M., Nomura,K., Numazaki,R.,
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequence of in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
properse.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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PUBMED
COMMENT
                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="NCI CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI_CGAP GC4 was prepared, and
se circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1228631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/liange/liange.html
Insert Length: 767 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA linear EST 06-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukamalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 388)
                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                              Hominidae, Homo.
1 (bases 1 to 365)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY019540 RIKEN full-length enriched, mammary gland RCB-0526 Jyg-MC(A) cDNA Mus musculus cDNA clone G830035L04 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inser program of the discontinuous seq primer: -400P from Gibco High quality sequence stop: 324.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
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                    sapiens (human)
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Query Match:
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BY019540/c
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ORGANISM
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AUTHORS
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                    SOURCE
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ORIGIN

DEFINITION

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31-DEC-2002
similar to
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Not1; Site_2: Xho1; cDNA made by oligo-dT priming.

Size-selected on agazose gel. Average insert size -1kb. 5'

Xho1 site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD, Mctabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, Mn 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@blohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae, Homo.

1 (bases 1 to 404)

1 (bases 1 to 404),

Methon, D.,

Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                  CA949507 404 bp mRNA linear EST iq25c06.x1 HR85 islet Homo sapiens cDNA clone IMAGE: 3' SW:FKHR_HUMAN Q12778 FORK HEAD DOMAIN PROTEIN FKHR. [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
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Matches:
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Mismatches:
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Matches:
Conservative:
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                   52 AladlyLeuProSerAlaSerAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (hinoue@im.wustl.edu)
Seg primer: -40RP from Gibco
High quality sequence stop: 401.
Location/Qualifiers
                                                                                                                                                    US-09-989-890-238 (1-212) x BE863674 (1-401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="IMAGE:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA949507.1 GI:27442384
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                          Percent Similarity:
Best Local Similarity:
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                                                                      Query Match:
DB:
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KEYWORDS
SOURCE
ORGANISM
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CA949507/c
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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| Organism="Musm musculus"
| wol_type="mrsh" |
| farain="C57BL/64" |
| farain="Unit mile management |
| farain="Vector: p777D-pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Bco RI; The NIH BMAP M SI |
| farain="Vector: p777D-pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Bco RI; The NIH BMAP M SI 1 Library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipocampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chin, H
National Institute of Mental Health
National Institute of Mental Health
National Institute Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 1706
Fax: 301 443 9890
Email: mESTGmmil.nih.gov
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BWAP CDNA clones from RESEARCH GENETICS. It
should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                               BE863674 1inear EST 29-SEP-2000 UI-M-BH0-akc-f-05-0-UI.rl NIH BMAP M S1 Mus musculus cDNA clone UI-M-BH0-akc-f-05-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 401)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                      388
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                                                                                                                     Conservative:
Mismatches:
Indels:
Gaps:
                                                                        Length:
Matches:
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                                                                                                                                                                                                                                                                                              52 AlaGlyLeuProSerAlaSerAlaAlaAla 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovery
Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                 US-09-989-890-238 (1-212) x BY019540 (1-388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 51
BE863674/c
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                   Pred. No.:
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PUBMED COMMENT

PEATURES

ORIGIN

AUTHORS TITLE JOURNAL

REFERENCE

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/Word_type="mrRNA"
// db_xref="mrRNA"
// db_xref="mrRNA"
// db_xref="mrRNA"
// db_xref="mrRNA"
// db_xref="mrRNA"
// db_bst="blio-akc-f-05-0-UI"
// ds_bst="blio-akc-f-05-0-UI"
// db_bst="blio-akc-f-05-0-UI"
// ds_bst="blio-akc-f-05-0-UI"
// ds_bst=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleoride that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Notl site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library CDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. POLYA=Yes.
                                                                                                                      AIB54714 14-05-0-UI.SI NIH EMAP_M_SI Mus musculus cDNA clone UI-M-BH0-akc-f-05-0-UI.3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Chin, H
Mational Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
Indels:
122 GCGGGCCTGCCCTCGGCCTCGCCGCT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .421
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                      A1854714.1 GI:5498620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 421)
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Fax: 301 443 9890
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
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PUBMED
COMMENT
                                                              RESULT 54
AI854714
                                                                                                                                                                                                                            ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DAA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/lmage/image.html

Insert Length: 790 Std Error: 0.00

Seq primer: -40RP from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Organism="Homo sapiens"
// wol_type="mRNA"
// wol_type="mRNA"
// db_tref="taxon:9606"
// clone="tMagE:2130482"
// lab_host="DH108"
// clone lib="NCI CGAP Kid11"
// clone lib="NCI CGAP Kid11"
// note="lorgan: kIdney; Vector: pT7T3D-Pac (Pharmācia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and se circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelbe 132376-1323911, 1456007-1456775, and 150052-1502855). Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                A1494178 13-APR-1999 til4g02.yl NCI CGAP Kidll Homo Bapiens CDNA clone IMAGE:2130482 5' similar to SW:FKHR_HUWAN Q12778 FORK HEAD DOWAIN PROTEIN FKHR. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
1 (bases 1 to 419)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419
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Matches:
Conservative:
Mismatches:
Mismatches:
Indels:
                                                                                                                                                                                        Gaps:
                                                                                                                                US-09-989-890-238 (1-212) x CA949507 (1-404)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI494178
AI494178.1 GI:4395181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
10.00
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4.7%
   100.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
   Best Local Similarity:
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Best Local Similarity:
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                                    Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                    RESULT 53
AI494178/c
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VERSION
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AUTHORS
TITLE
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FEATURES

COMMENT

SOURCE

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421 10 0 0 0 0

Gaps:

52 AlaGlyLeuProSerAlaSerAlaAlaAla 61

ORIGIN

Score:

us-09-989-890-238.oligo_p2n.rst

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

PEATURES

RESULT 55 A1188507/c DEFINITION

g ሯ

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/clone lib="NGI CGAP Kidl2"
//clone lib="NGI CGAP Kidl2"
//note="Organ: kIdney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: ECO RI; Plasmid DNA from the normalized library NCI CGAP Kids was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW420053 460 bp mRNA linear EST 09-FEB-2000 fj86g08.yl zebrafish gridded kidney Danio rerio cDNA 5', mRNA sequence.
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                           Hominidae, Homo.

1 (bases 1 to 459)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2873162"
/tissue_type="2 pooled tumors (clear cell type)"
/lab host="DH108"
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0 0 0 0
0 0 0
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Possible reversed clone: polyT not found Seg primer: -400P from Gibco High quality sequence stop: 445.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaGlyLeuProSerAlaSerAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-989-890-238 (1-212) x AW467069 (1-459)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio (zebrafish)
                         GI:7037175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:6947985
                                                               Homo sapiens (human)
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AW467069.1
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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KEYWORDS
SOURCE
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                                                                                                                                                                                     AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 bp mRNA linear EST 24-FEB-2000 ha09a02.x1 NCI CGAP Kidl2 Homo sapiens cDNA clone IMAGE:2873162 3' similar to SW:FKGR HUMAN Q12778 FORK HEAD DOWAIN PROTEIN FKGR. [1] ;, mRNA sequence.
                                                                                                                                                                  EST 28-OCT-1998
                                                                                                                                                     qd14e10.x1 Soares_placenta_8to9weeks_2NbHP8to9W.Homo sapiens cDNA clone IMAGE:1723722 3' similar to SW:PKHR_HUMAN Q12778 FORK HEAD DOMAIN PROTEIN FKHR.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 434)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs -r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the IMAGB Consortium (infr@mimage.llnl.gov) for further information. Insert Length: 713 Std Brror: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 417.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                   323 GCTGGCTAGTGCCAGCGCTGCTGCG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 GCGGCCTGCCCTCGGCCTCGGCTGCCGCT 102
                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AlaGlyLeuProSerAlaSerAlaAlaAla 61
                                          52 AlaGlyLeuProSerAlaSerAlaAlaAla
US-09-989-890-238 (1-212) x AI854714 (1-421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-989-890-238 (1-212) x AI188507 (1-434)
                                                                                                                                                                                                                                                                   AI188507.1 GI:3739716
                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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10.00
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .434
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Query Match:
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RESULT 56 AW467069/c LOCUS DEFINITION

ò 셤

Pred. No.:

ORIGIN

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/ Organishm="now" bagining
/ Organishm="mRNA"

/ Ab_xref="taxon:9606"
/ Clone="IMAGRS:6546952"
/ (issue type="Purified pancreatic islet"
/ lab_host="DH10B"
/ clone lib="HRBS islet"
/ clone lib="HRBS islet"
/ note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/ note="Organ: pBluescript SK(-); Site_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 504)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Characteristics of the Lotus japonicus gene repertoire deduced from large-scale expressed sequence tag (EST) analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 19-AUG-2004
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Stragtota, Viridiplantae; Stregtotohyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Cachatta, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tasgareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Badocrine Pancreas Consortium Bowers, Y. Unpublished (2000)

Contact: Douglas Melcon, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Bravard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
                                                                                                                                                                                                                                                                                                                                                                                               Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Mashington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV780819 504 bp mRNA linear EST 19-AU AV780819 Lotus japonicus Pods (20-30 mm in length) Lotus corniculatus var. japonicus cDNA clone MPDL083d04_£ 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (hinoue@im.wustl.edu)
Seg primer: -40RP from Gibco
High quality sequence stop: 439.
Location/Qualifiers
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488 bp mRNA linear EST 30-DEC-2002 il:33b08.X1 HR85 islet Homo sapiens cDNA clone IMAGE:6546952 3' saimilar to SW:FKHR_HUMAN Q12778 FORK HEAD DOMAIN PROTEIN FKHR. [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="kidney pooled from 300 wild type adults" /lab_host="XzbzRish gridded kidney" /clone_lib="zebrafish gridded kidney" /note="Organ: kidney; Vector: pBK-CMV; Site_1: EcoRI; Site_2: KhOI; Oligo dT cDNA library constructed from mRNA pooled from pooled kidney tissue from 300 adult zebrafish."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address:
www.resgen.com) (email contact: info@crsgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                          Cypriniformes; Cyprinidae; Danio.

(Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Milson, R.

Waterston, R. and Milson, R.

WashU Zebrafish EST Project 1998
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 488)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                                                                                                                                                                                                                                                                                                                                                             Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
          Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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/mol_type="mRNA"
/db xref="taxon:7955"
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High quality sequence stop: 426.
Location/Qualifiers
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CA941290.1 GI:27429770
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Homo sapiens
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us-09-989-890-238.oligo_p2n.rst

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BH298354 100V-2001 CH230-146C24.TVB CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-146C24, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Remain" | Coll Lype="Brain" | Coll Lype=
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Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bnamaalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus,
1 (bases 1 to 557)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregeorgia, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Matches:
Conservative:
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/organism="Rattus norvegicus"
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-146C24"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
                                                                                                                                                         Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF434989 511 bp mRNA linear EST 29-NOV-2000
Typ04604.x1 NCI CGAP OV18 Homo sapiens cDNA clone INAGE:3644910 3'
similar to SW:FGHR HUMAN Q12798 FORK HEAD DOMAIN PROTEIN FKHR. [1]
;contains MER22.t2 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                  /organism="Lotus corniculatus var. japonicus"
/mol type="mRNA"
/isolate="Miyakoina MG-20"
/db xref="thaton:34305"
/clone="MPDL083404 f"
/tissue_type="Pods [(20-30 mm in length)"
/clone lib="Lotus japonicus Pods ((20-30 mm in length)"
/clone lib="Lotus japonicus Pods ((20-30 mm in length)"
/note="Vector: pBluescriptII SK-; Site_I: BcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases | to 511)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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0 0
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/tissue type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                 The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
      Mol. Biol. 54 (3), 405-414 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 GCACTTCCATCTTCCCTTGCCTCTCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 AlaLeuProSerSerLeuAlaLeuLeuSer 32
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                       Contact: Brika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
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100.0%
100.0%
4.7%
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         Plant Mol
15284495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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KEYWORDS
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TITLE
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ORIGIN

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CK691303 576 bp mRNA linear EST 30-MAR-2004
ZF101-P00055-DEPE-F2 009 GISZF001_ra Danio rerio cDNA clone
IMAGE:7155107 5', mRNA sequence.
                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Meoperygii, Teleostei, Ostariophysi, Cypriniformes; Cyprinidae, Danio.

(Cypriniformes; Cyprinidae, Danio.

(Dases 1 to 576)

Wei, C., Mathavan, S., Thoreau, H., Lim, L., Lee, C. and Ruan, Y. Genome Institute of Singapore, Zebrafish Gene Collection Unpublished (2004)
                                                                                                                                                                                                                                                                                                          Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
Tal: +65 6478 8073
Fax: +65 6478 9059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576
10
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
/mol_type="mRNA"
/mol_type="mRNA"
/db_train="Singapore local strain"
/db_traf="texon:7955"
/clone="IMAGE:7155107"
                                                                                                                                                                                                                                                                                                                                                                                 Email: ruany/@gis.a-star.edu.sg
GIS Clone ID: ZF101-P00055-BR2_009
PCR PRIMERS
FORWARD: M13
BACKWARD: M13
BACKWARD: M13
Seq primer: CCGCATAACTTGTATAGCA
High quality sequence stop: 576.
224 TCTGGAGCTGGGCTTCCTAGTGCGTCGGCC 195
                                                                                                                  CK691303
CK691303.1 GI:42443639
                                                                                                                                                             Danio rerio (zebrafish)
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10.00
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Pred. No.:
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VERSION
KEYWORDS
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                                                                                     DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                            RESULT 63
                                                           CK691303
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ZMMBBb0108F12.r ZMMBBb Zea mays genomic clone ZMMBBb0108F12 3',
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD Calde, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 560)

Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Pax: 520 621 9288
Email: rwing@genome.arizona.edu
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Matches:
Conservative:
Mismatches:
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Indels:
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                                                                                                                                                                                            25 ProSerSerLeuAlaLeuLeuSerArgPro 34
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                                                                                                                                Gaps:
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/mol type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                             US-09-989-890-238 (1-212) x BH298354 (1-557)
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Seg primer: M13r
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4577"
/clone="ZMMBBb0108F12"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing of the maize genome Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                      genomic survey sequence.
CC740775
CC740775.1 GI:32193228
GSS.
 Pieter de Jong"
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                                                                                    Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
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Zea mays
                                            Alignment Scores:
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DB:
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CC740775/c
LOCUS
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VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
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AUTHORS
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CE564205.1 GI:36880986 GSS.
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10.00
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Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Evarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 597)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Direct Submission
                                                                                                                                                   Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN145101, genomic survey sequence. CR1811960. CR1811960. GI:49960809 GSS; genome survey sequence; MICER. Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.

Hominidae, Homo.

Loases 1 to 600)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597
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Mismatches:
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Mismatches:
Indels:
Gaps:
                                                                                                       351 AGCCTAGCATTGTTATCAAGACCGTTGAGC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 AlaGlyLeuProSerAlaSerAlaAlaAla 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="WHPN145i01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-989-890-238 (1-212) x CR181960 (1-597)
                                                           US-09-989-890-238 (1-212) x CK691303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
10.00
100.0$
100.0$
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 Local Similarity:
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Query Match:
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CR181960/c
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JOURNAL
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                   REPERENCE
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/clone lb="NCI CGAP Kidl1"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Bco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (Gloneids 1322376-1323911, 1456007-1456775, and Fatima Bonaldo. "Subtraction by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          605 bp DNA linear GSS 28-SEP-2003
tigr-ges-dog-17000327503738 Dog Library Canis familiaris genomic,
GESE4205
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
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Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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autu nayabutzani, i.

autu nayabutzani, i.

autu nayabutzani, i.

sequencing pipeline with 384 multicapillary sequencer. Genome Res. .

10 (11), 1757-1711 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsunra, S., Kawal, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Mus. Sciurognathi; Muroidea; Murinae; Mus. Sciurognathi; Muroidea; Murinae; Mus. Bases I to 620)

8. Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Saito, R., Sakai, C., Sakai, C., Sano, H., Sasaki, D., Shibata, K., Sato, H., Sakai, T., Sogabe, Y., Suuki, H., Tagami, M., Tagawa, A., Fakahashi, F., Taken Mouse ESTs (Arakawa, T., Poya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB659723 RIKEN full-length enriched, 13 days embryo lung Mus musculus cDNA clone D430004P20 5', mRNA sequence.
                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                    122 TTACTCTCCCGCCCTCTCTCTCCCCCCTCA 93
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  (0) 1.34.65.22.73"
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BB659723.1 GI:16493544
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                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                   Alignment Scores:
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DB:
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                               Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EX871243 tcbk Oncorhynchus mykiss cDNA clone tcbk0019c.c.19 5prim, mRNA seguence.
EX871243 GI:42785983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Sukaryota; Metazoa; Ghordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases I to 618)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
Unpublished (2013)
On Dec. 17, 2003 this sequence version replaced gi:39994830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=_vector: pT7T3D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre. Francois PIUMI,
Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
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/note=_Site_l: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INRA - SCRIBE
Campus de Deaulieu, RENNES cedex, 35042, France
Trl: 02.23.48.50.09
Fax: 02.23.48.50.20
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                                                                                                         organism="Canis familiaris"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 LeuLeuSerArgProLeuSerProProPro 39
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Seq primer: M13R.
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Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
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10.00
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Query Match:
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Pred. No.:
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BX871243/c
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KEYWORDS
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TITLE
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                                                         FEATURES
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mismatches:
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Matches:
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DB:
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KEYWORDS
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ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                                            B1824376 647 bp mRNA linear EST 04-0CT-2001
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                             /dev stage="13 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LiAMil447 row: d column: 01
High quality sequence stop: 644.
Location/Qualifiers
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1 (bases 1 to 647)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapber@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                       'organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1-620)
                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D430004P20"
  Location/Qualifiers
                                                                                                                                                             tissue_type="lung"
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BM265585 619 652 bp mRNA linear BST 18-DEC-2001 fw57d06.yl Sugano SJD adult male Danio rerio cDNA clone IMAGE:5611811 5' similar to TR:Q9Y4E0 Q9Y4E0 KIAA0595 PROTEIN ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_grage="mature"
/clone lib="Zebrafish Kidney Marrow cDNA library"
/clone lib="Zebrafish Kidney Warrow cDNA library"
/note="Organ: kidney; Vector: pBS-CMV; Site_1: Xho!;
Site_2: EcoRI; Total RNA was extracted from the kidney
tissues of mature zebrafish. The poly (A) + RNA fraction
was separated from total RNA by oligo (dT) cellulose
chromatography. Library was initially constructed in the
lambdaZAP Express vector (Stratagene) and in vivo excised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Ospriniformes; Cyprinidae; Danio.

1 (bases 1 to 652)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Bddy,S., Hillier,L., Kucaba,T., Martin,G., Beck,C., Wyle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Wasturston,R. and Wilson,R.
     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.

(Cypriniformes, Cyprinidae, Danio.

(Charles I to 650)

Song, M.D., Sun, X.J., Deng, M., Zhang, G.W., Zhou, Y., Wu, X.Y., Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Zon, L.I., Kanki, J.P., Liu, T.X., Look, A.T. and Chen, Z.

Hematopoietic gene expression profile in zebrafish kidney marrow Proc. Natl. Acad. Sci. U.S.A. 101 (46), 16240-16245 (2004)
                                                                                                                                                                                                                                                                                 Contact: Chen Z.
Contact: Chen Z.
State Key Lab for Medical Genomics
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University
197 Rui Jin Road II, Shanghai 200025, P. R. China
Tel: 86-21-64744040
Fax: 86-21-64743206
Email: zchen@stn.sh.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Danio rerio"
/mol_type="mRNA"
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/clone="RK114A2E10"
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BM265585
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Concessive 1: Sall; Site 2: Bamil; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genomic Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGAACCATCTTTTTTTTTTTTTTTTTT S), cDNA was prepared by using trebalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 479.0. Second strand cDNA was prepared with the primer adapter of strand cDNA was prepared with the primer adapter of strand cDNA was cleaved with XNOI and Bamil. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
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RK114A2E10.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA clone RK114A2E10 5', mRNA sequence.
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Hayashizaki, Y., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Labbratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                    Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="cerebellum"
/dev stage="0 day neonate"
/lab_host="DH10B"
/clone llb="RIKEN full-length enriched, 0 day neonate
cerebellum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="C230083P08"
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CD598528.1 GI:31779880
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Conservative: Mismatches: Indels:

Matches:

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Homo sapiens (human)
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4.7%
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/tissue_type="whole body"
/tissue_type="whole body"
/dev stage="adult"
/lab host="DH108 (phage resistant)"
/clonellb="Sugano SJD adult male"
/clonellb="Sugano SJD adult male"
/note="Vector: pMENBS-FL3; Site 1: DraIII (CACCATGTG);
Site_2: DraIII (CACTGTGTG); lst strand cDNA was primed
with an oligo(dT) primer [ATGTGCCTTTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TGTTGGCTRCTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG: Xhol should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed and donated by Dr. Sumio
Sugano (University of Tokyo Institute of Medical Science).
CUSTCTGCTGTRAAAGTGG and 3' end primer
CTGTCTGCTGTRAAAGTGG and 3' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR976136 CR976136 659 bp mRNA linear EST 22-JUN-2005 CR976136 RZPD no.9016 Homo sapiens cDNA clone RZPDp9016D1639 5', mRNA sequence.
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 659)
Heil, O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D. and Korn, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                        1. .652
/organism="Danio rerio"
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                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5611811"
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Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                          /sex="male"
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Homo sapiens
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100.0%
4.7%
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SOURCE
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CR976136
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COMMENT
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RZPDILB; (Human T-Lymphocytes) RZPD LIB No.9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
Inge Arlart
RZPD Dettsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9016D1639
contact RZPD (product - support@rzpd.de) for further information.
Primer name: qg31 4, Primer sequence: CGGATAACAATTCACACAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM051939 668 bp mRNA linear EST 07-NOV-2001
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 668)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
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Matches:
Conservative:
Mismatches:
Indels:
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPD99016D1639.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RZPDp9016D1639"
/tissue_type="T-Lymphocytes"
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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Hominidae, Homo.

B. (Dases I to 695)

S. Inu, X., Porter, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Lingubly X., Jay, G. and He, W.
High-throughput cloning of full-length human cDNAs directly from
Contact: Keyacs, KF
High Throughput CDNA Cloning
Origene Technologies, Inc. (www.origene.com )
Corlader Technologies, Inc. (www.origene.com )
Criden Technologies, Inc. (www.origene.com )
Fart Sol 340 3188
Fax: 301 340 8606
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FORDER TOTAL BANDA TARGE INSERT, DOMY expression library lemon sapiens cDMR clone TC118890 5' similar to Homo sapiens for (Forder Forder Fo
/lab host="DH10B (phage-resistant)"
/clone_lbb="NIH_MGC_B"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: BcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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This EST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.
Please contact OriGene for access.
OriGene Technologies, Inc.
6 Tafk Ct. Suite 100
ROCKVille, MD 240-3188
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/clone lib="Human fetal brain, large insert, pCMV
expression library"
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Seg primer: pCNV6 Sprime forward vector primer, OriGene
Technologies Inc.
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="TC118890"
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DR001418.1 GI:66261291
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DR001418
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AUTHORS
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                                                                                                                                                                                    BM051456 686 bp mRNA linear EST 07-NOV-2001 603638116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5419510 5',
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llni.gov
Plate: LLCM1872 row: o column: 03
High quality sequence stop: 685.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:
http://image.llml.gov
Plate: LLCM1873 row: b column: 11
High quality sequence stop: 664.
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1 (bases 1 to 686)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/tissue_type="Burkitt lymphoma"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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ORGANISM
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AUTHORS
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JOURNAL
COMMENT
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KEYWORDS
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ORIGIN

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/clone="Integration of the property of the pro
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF727607
UI-M-HBO-CKi-h-12-0-UI.x1 NIH_BMAP_HBO MUS mUSCUluS CDNA clone
IMAGE:30548435 5', mRNA sequence.
/note="Organ: Fetal Brain; Vector: pCMV6-XL4; Site 1: EcoR1; Site_2: Xhol/Sall compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRMA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector. random clones selected for end sequence verification of full-length genes"
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: pYX-5.
Location/Qualifiers
1.702
A.coganism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-989-890-238 (1-212) x DR001418 (1-695)
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CF727607.1 GI:37601775
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AUTHORS
TITLE
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COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Buteleostei; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Euteleostei; Libasea Lto 705; Eleostei; Lossea Lto 705; Eleostei; Lossea Lto 705; Eleostruction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss Unpublished (2003)

D. Dec 18, 2003 this sequence version replaced gi:40140704. Contect: Guiguen Y INRA - SCRIBE Campus de beaulieu, RENNES cedex, 35042, France Tel: 02.23.48.50.09

Fax: 02.23.48.50.09

Fax: 02.23.48.50.09

Email: Yann.Guiguenobeaulieu.rennes.inra.fr Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX890304 tcbk Oncorhynchus mykiss cDNA clone tcbk0033c.k.12 5prim,
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in th
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cloud lib="Chick"
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/cloud lib="Libb"
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mulii-triseues - normalized + 2 subtractions; Clone
distribution: AGENAE Resource centre. Francois Plumi,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Joaga cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.705
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                                                                                                                            702
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Matches:
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus mykiss (rainbow trout) Oncorhynchus mykiss
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                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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TITLE
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KEYWORDS
SOURCE
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/note="vector: pBlueScript II sk(+) XR; Site_1: EcoRI;
/note="vector: pBlueScript II of gram medium for 96
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/nous. Cultures were vacuum filtered and the mycelial mats
/nous. Cultures were vacuum filtered and the mycelial mats
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/nous. Cultures v
                                                                                                                                                                                                                                                                                                 711 bp mRNA linear EST 11-JUL-2005 FvG Gibberella moniliformis cDNA clone FVGCK02, mRNA
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;

Hypocreomycotetidae, Hypocreales, Nectriaceae, Gibberella.

1 (bases 1 to 711)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Rendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)
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Fax: 309 681 6689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Gibberella moniliformis"
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/strain==m3125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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TIGR sequence name: FVGCKOZTH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
Location/Qualifiers
                                                                                                                                301 GCTGGGCTGCCTAGTGCCAGCGCTGCTGCG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33
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                                                                                                    52 AlaGlyLeuProSerAlaSerAlaAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLeuSerArgProLeuSerProPro
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                               JS-09-989-890-238 (1-212) x CB246007 (1-710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibberella moniliformis
                                                                                                                                                                                                                                                                                                                                                                                                                                        DR608449.1 GI:70683097
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EST998577 E
                                                                                                                                                                                                                                                                                                                                                                      sequence.
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/clone_lib="NHL BMAP state in the lip-odr primed with Containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Bcok I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGAGCC. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                           UI-M-FOO-cdu-n-21-0-UI.rl NIH BMAP_FOO Mus musculus cDNA clone IMAGE:6834742 5', mRNA sequence.
CB246007
ES746007.1 GI:28367651
EST.
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Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                       LeuLeuSerArgProLeuSerProProPro 39
                                                                                                                                                                                                         122 TTACTCCCGCCCTCTCTCCCCCTCCA 93
   Indels:
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                                                                                                    US-09-989-890-238 (1-212) x BX890304 (1-705)
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/strain="C57BL/6"
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Mus musculus
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4.78
                                                                                                                                                                       30
   Query Match:
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CB246007/c
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VERSION
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TITLE
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DR614353 714 bp mRNA linear EST 11-JUL-2005 EST1004481 FvH Gibberella moniliformis cDNA clone FVHBF85, mRNA

DEFINITION

RESULT 81 DR614353

710 0 0 0

Matches: Conservative: Mismatches: Indels:

10.00 100.0% 100.0% 4.7%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

Score:

Length:

g

603 CTCCTTTCAAGACCACTTTCGCCGCCACCT 632

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Maruelia, Eutheria; Buarchontoglires; Glires; Rodentia; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Murinae; Rattus.

1 (bases 1 to 721)

2 Lao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shatsman, S., Tsegaye, G., Geer, K., Rissell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

L Unpublished (1999)

Other GSSs: CH230-68M10.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH230-68M10.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-68M10, genomic survey sequence.
                                                                                                     Zea maýs
Skaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4577"
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/note="Vector; pCR4-TOFO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                                                                                                                                                                                                             1 (bases 1 to 714)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
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Mismatches:
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUHBS30TD
Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: whitelaw@tigr.org
Seg primer: TR
Class: sheared ends.
                              GI:30935023
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// organism="Gibberella moniliformis"
// mol_type="mRNA"
// strain="mal15"
// firsh="mal15"
// db_xref="raxon:117187"
// clone="Tub
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                                                                                                                      Gibberella moniliformis

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycotedidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 714)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)

Contact: Brown, D.W.
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1815 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVHBF85TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
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                                                    DR614353.1 GI:70689001
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BX913421
BX913421.2 GI:43422650
Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plater: 68 row: M column: 10

Seg primer: T7

Class: BAC ends.
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Oncorhynchus mykiss
Oncorhynchus mykiss
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
I (bases I to 734)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
Inbraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Jan 22, 2004 this sequence version replaced gi:41130229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
//olone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SBNHBd/MCW) BĀC library produced by
Pieter de Jong"
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Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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/mol_type="genomic DNA"
/strain="NN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-68M10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 CCATCCAGCTTAGCTCTTCTCCCAGACCC 264
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Seg primer: M13R.
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BX913421/c
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                                                                                                                                                                                                                                                                                                                                                                   /notes="Vector: pT713D-pac; AGENAE Rainbow trout multi-tissues - normalized + 2 subtractions; Clone distribution: AGENAE Resource centre. Francois PIUMI, Francois Piumi@jouy.inra.fr, INRA, CER Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Joass cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

(bases 1 to 724)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y. Kendra, D.F., Town, C. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Contact: Brown, D.W.

UNDADARS/NCAUR.
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Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVGBCIBTH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
Location/Qualifiers
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/mol_type="mRNA"
/strain="m3125"
                              /mol_type="mana"
/db_xref="taxon:8022"
/clone="taxon:8022"
/tistue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
organism="Oncorhynchus mykiss"
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Gaps:
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/clone_lib="FvG"
                                                                                                                                                                                                                                                                                                                                clone_lib="tcbk"
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10.00
100.0%
100.0%
4.7%
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Oncorhynchus mykiss (rainbow trout)

Oncorhynchus mykiss

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopteryota; Meopterydi; Teleostei; Buteleostei;

Actinopterygi; Salmoniformes; Salmonidae; Oncorhynchus.

E (bases it of 726)

G Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA

Ilbraries in rainbow trout, Oncorhynchus mykiss

U Mpublished (2003)

On Jan 22, 2004 this sequence version replaced gi:41129432.

Contact: Guiguen Y

INRA - SCRIBE

Campus de beaulieu, RENNES cedex, 35042, France

Tel: 02.23.48.50.09

Fax: 02.23.48.50.09

Fax: 02.23.48.50.00

Email: Yann.Guiguenebeaulieu.rennes.inra.fr

Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK6888994 1733 bp mRNA linear EST 30-MAR-2004
ZF101-P00047-DEPE-F2_M04 GISZF001_ra Danio rerio cDNA clone
IMAGE:7151982 5', mRNA sequence.
                                                          BX912624 Tcbk Oncorhynchus mykiss cDNA clone tcbk0072c.f.19 5prim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib-rtcbk.
/clone lib-rtcbk.
/note="Vector: pT7T3D-pac, AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution: AGENAE Resource centre. Francois PIUMI,
Francois:Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genôme (LREG), Domaine de Vilvert, 78352,
Jouy-en-Joses cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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/clone="tcbk0072c.f.19"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH108"
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Conservative:
Mismatches:
Indels:

    .726
    /organism="Oncorhynchus mykiss"

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BX912624
BX912624.2 GI:43420585
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EST.
Danio rerio (zebrafish)
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Best Local Similarity:
Query Match:
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DEFINITION
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AUTHORS
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CK688894
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PUHBSJOTD ZM 0.6 1.0 KB Zea mays genomic clone ZMWBTa415E11,
genomic survey sequence.
then added to TRIzol Reagent (Invitrogen, Carlsbad CA) at approximately 1 g mycelia per 10 ml TRIZOl. The CDNA was directionally ligated into the pBlueScript II SK(+) XR vector (CDNA Synthesis Kit; Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bepranciphyta, Bagnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 724)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="ZM 0.6 1.0 KB"
/note="Vector: pcR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                             (1-724)
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/clone="ZMMBTa415E11"
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Class: sheared ends.
Location/Qualifiers
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Other GSSs: PUHBS30TB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC437178 CC437178.1 GI:30935027
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192
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Zea mays
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Pred. No.:
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KEYWORDS
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AUTHORS
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CC437178
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JOURNAL
COMMENT
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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CF386451 T4 A09.gl A015 Loblolly pine roots recovering from drought DR1 Pinus taeda cDNA clone RTDR1_14_A09_A015 5', mRNA sequence.
CE265375
tigr-gss-dog-17000336935657 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopaida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 749)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
                                                                                                                                                                                                                                                                                                      Kirkness E.F., Bain, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/Btrain="Standard Poodle"
/db_xrefi="taxon:9615"
/db_xrefi="taxon:9615"
/clone lib="bog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                   The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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Unpublished (2003)
Other ESTS: RIDR1_14 A09.bl A015
Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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/organism="Canis familiaris"
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Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ekirknes@tigr.org
                                                       genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CF386451.1 GI:34344786
                                                                                                    CE265375.1 GI:35986194
                                                                                                                                                 Canis familiaris (dog)
Canis familiaris
                                                                                                                                                                                                                                                                                   (bases 1 to 744)
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Fax: 301-838-0208
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// Organisms="Sangapore local strain"
// db xref="caxon:1955"
// clone="IMAGE:7151982"
// tissue_type="Embryo"
// dev stage="TD Different embryonic Stages(From just fertilized Embryos to 72 hours just hatched baby fish)"
// lab_host="DH10B"
// clone=11b="GISZFOOL ra"
// clone=11b="GISZFOOL ra"
// clone=12: Sfi B (GGCGGGGGGCG); Priming method: Sfi-(dT)30
Primed; Priming sequence:
// note="Vector: pDNR-LIB; Site 1: Sfi A (GGCCATACGCC);
Site_2: Sfi B (GGCCGAGGCGGCCAAG(T)30N ; Directionally
cloned, S' cloning site: Sfi A site GGCCATACGCC;
S' ATTCTAGAGGCCGAAGCGCGCAAG(T)30N ; Directionally
cloned, S' cloning site: Sfi B site GGCCAAGGTGGCC;
Inker/adaptor sequence: S.AAGCAGGGGCGC;
// cloning site: Sfi B site GGCCGAAGGTGGCC;
// cloning site: Sfi B site GGCCGAAGGTGCC;
// cloning site: Site GGCCGAAGGTGCC;
// cloning si
               Cloning and Sequencing
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
Tel: +65 6478 8073
Fax: +65 6478 9059
Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZF101-P00047-BR2_M04
FCR PRIMER:
FORWARD: M13
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Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: M13
Plate: ZF101-P00047-BR2 row: M
Seq primer: CCGCATAACTTGTATAGCA
High quality sequence stop: 733.
Location/Qualifiers
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source

FEATURES

JOURNAL

432 AGCCTAGCATTGTTATCAAGACCGTTGAGC 461

CE265375/c

RESULT 89

셤 à

Query Match: DB:

Pred. No.:

ORIGIN

COMMENT

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DR647955 757 bp mRNA linear EST 12-JUL-2005 EST1038072 FvN Gibberella moniliformis cDNA clone FVNAD49, mRNA
                                                                                                                                                                                                                                                                                                                 /tissue type="mycelia"
/clone lib="rvN"
/clone lib="rvN"
/note="vyctor: pBlueScript II SK(+) XR; Site_1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioIdes. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M.3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
condia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dashes,
and incubated at room temperature for four or six days."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Fungi, Asconycota, Pezizomycotina; Sordariomycetes, Hypocreomycetidae: Hypocreales; Nectriaceae; Gibberella.

I (bases I to 77).

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y. Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Uppublished (2005)

Contact: Brown, D.W.
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Fax: 309 681 6689
Email: browndowncaur.usda.gov
TIGR sequence name: FVNND49TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
Location/Qualifiers
                                                                                                                            1. 749
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNB408"
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/organism="Gibberella moniliformis"
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Matches:
Conservative:
Mismatches:
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVNB408TH
Seq primer: AAT TAA CCC TCA CTA AAG GG.
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strain="m3125"
/db_xref="taxon:117187"
/clone="FVNAD49"
/tissue_type="mycelia"
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                                                                                                                        Email: mmpratt@dg.edu

RNA prepared and library constructed by W. Walter Lorenz, School of

Forestry, University of Georgia; plant material prepared at the

Forestry of Florida; sequencing done in the Laboratory for

Genomics and Bioinformatics, University of Georgia. Sequence ends

have been trimmed to exclude vector and regions below Phred quality

16. Three-prime sequences are presented as their reverse complement

and have been trimmed to exclude polyA.

Seq primer: JENNEY (CAGGAAACAGCTATGACC).
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1 (Bases I to 749)

1 (Bases I to 749)

1 (Bases I to 749)

1 (Chases I to 749)

2 (Chases I to 749)

3 (Chases I to 749)

4 (Chases I to 749)

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5 (Chases I to 749)

6 (Chases I to 749)

7 (Chases I to 749)

7 (Chases I to 749)

8 (Chases I to 749)

9 (Chases I to 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="vector: pSL1180; Site 1: ECORI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots recovering from drought. Water was withhold from ramet clones until predawn needle water potential reached -1.75 MPa. Plants were well watered on day 7 and allowed to recover for 2 days, at which time roots were harvested for RNA isolation. Double-stranded CDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Loblolly pine roots recovering from drought DRI"
The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:3352"
/clone="RTDR1 14_A09_A015"
/lab_host="DH108-T1 phage-resistant E. coli"
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Tel: 309 681 6230
Fax: 309 681 6689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
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DR652062.1 GI:70740538
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University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 335 9250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Provasoli-Guillard National Center for Culture
of Narine Phytoplankton (CCMP)
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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CDNA Library Arrayed by: Dr. M. Bento Soares
CDNA Library Arrayed by: Dr. M. Bent
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/#strain="cCMP 371"
//be xref="taxon:293"
/cloine="tul-reH-do-aak-o-08-0-UI"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/cloine lib="UI-BH-HG0"
/note="Vector: pT713-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR 1; Site 2: Not 1; The library was
constructed according to Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CX773156

UI-EH-HGO-aak-o-08-0-UI.81 UI-EH-HGO Emiliania huxleyi cDNA clone
UI-EH-HGO-aak-o-08-0-UI 3', mRNA sequence.
/clone_lib="FvN"
/note="Vector: pBlueScript II SK(+) XR; Site I: BCoRI;
/note="Vector: pBlueScript II SK(+) XR; Site I: BCoRI;
/ste_2: XhoI; anamorph: Fusarium verticillioIdes. Library
FvN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
condia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."
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1 (bases 1 to 758)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory for Computational Genomics
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/organism="Emiliania huxleyi"
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CX773156.1 GI:58183509
EST.
Emiliania huxleyi
Emiliania huxleyi
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KEYWORDS
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Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAAAGGCTAGT. Tissue was obtained from the provasoli-Guillard National Center for Culture of Marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR646867 760 bp mRNA linear EST 12-JUL-2005 EST1036984 FvN Gibberella moniliformis cDNA clone FvNA630, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /notes __vector: pBlueScript II SK(+) XR; Site 1: EcoRI; Site 2: XhoI; anamorph: Fusarium verticillioides. Library FVN was obtained from RNA derived from a corn meal medium culture of strain M.3125. These cultures were prepared by inoculating an autoclaved mixture of 25 g corn meal and 5 ml distilled water with 5 ml of water containing 5 x 10e7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases I to 760)

2 (bases I to 760)

3 (bases I to 760)

4 (bases I to 760)

5 (bases I to 760)

5 (bases I to 760)

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TAG TISSUE-Emiliania huxleyi coccolithophorid
TAG_LIB=UI-EH-HG0
TAG_SEQ=GAAGGCTAGT"
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Tel: 309 681 6230
Fax: 309 681 6689
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Matches:
Conservative:
Mismatches:
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TIGR sequence name: FVNA630TH
Seq primer: AAI TAA CCC TCA CTA AAG GG.
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/clone_lib="FvN"
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/strain="m3125"
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Rattus norvegicus

Retus norvegicus

Retus norvegicus

Retus norvegicus

Retus norvegicus

Retus norvegicus

Sciurognathi; Murcidea; Muridae; Murinae; Rattus.

Sciurognathi; Murcidea; Muridae; Murinae; Rattus.

RS NIH-MCC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

AL Oppublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

National Cancer Genomics

National Cancer Cancer Genomics

Contact: Daniela S. Gerhard, Ph.D.

National Cancer Institute / NIH

Bldg. 31 RanlaNo? Bethesda MD 20892

Email: cgapbe-rémail.nih.gov

Tissue Procurement: Howard Jacobs

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be fround through the I.M.A.G.E. Consortium/LIML at:

Lucation/Qualifiers

1. 769

| Alpha quality sequence stop: 491. |

| High quality sequence stop: 491. |

| Location/Qualifiers |
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- bpArchacArcacAccaccaccaccacc(T) 25-3' and cloned into
the EcoRV/Norl sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 2.2 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 215) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH_MGC library."
condia. The inoculated medium was mixed thoroughly, distributed equally into two 100-mm plastic petri dishes, and incubated at room temperature for four or gix days."
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This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ180749 783 bp mRNA linear EST 30-APR-2002 UI-M-EXO-bxc-o-01-0-UI.rl NIH_BMAP_EXO Mus musculus cDNA clone IMAGE:5706456 5', mRNA sequence.
769
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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/organism="Wus musculus"
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/strain="C57BL/6"
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Mus musculus
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Pred. No.:
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DR656203 785 bp mRNA linear EST 12-JUL-2005 EST1046320 FvN Gibberella moniliformis cDNA clone FVNBU54, mRNA
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(bases 1 to 785)

Brown, D. W., Cheung, F., Proctor, R. H., Butchko, A. E., Zheng, L., Lee, Y. Utterback, T., Smith, S., Feldblyuw, T., Glenn, A. E., Plattner, R. D., Rendra, D. F., Town, C. D. and Whitelaw, C. A.

Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)

Contact: Brown, D. W.
                                                                                                                                                                                                                                                                                                                                                                            Gibberella moniliformis
Gibberella moniliformis
Bukaryota, Pungi, Ascomycota, Pezizomycotina, Sordariomycetes,
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Fax: 309 681 6689
Email: brownd@ncaur.usda.gov
TIGR sequence name: FVNBU54TV
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

    .785
    /organism="Gibberella moniliformis"
/mol type="mRNA"
/strain="m3125"

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                                                                           60 AlaAlaGlyIleAlaSerSerAlaValGlu
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                            US-09-989-890-238 (1-212) x CK478920 (1-783)
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/clone_lib="FvN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institutes of Health, Mammalian Gene Collection (MCC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Coffice of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
CDNA Library Preparation: Express Genomics
CDNA Library Preparation: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Location/Qualifiers
Ince / Arraye="mRNA" | Arraye" | Arraye" |
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                                                                                                                                                                                                                                                                                                                                               CK478920 783 bp mRNA linear BST 14-JAN-2004 AGENCOURT 17582913 NIH MGC_232 Rattus norvegicus CDNA clone IMAGE:7121341 5', mRNA sequence.
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- Portorachregoreaccec(T) 25-3' and cloned into the EcoRV/Not1 sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.3 kb. This primary library is normalized (non-normalized primary library is NIH MGC 211) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus sukaryotas (Laniata, Vertebrata, Euteleostomi, Bukaryotas, Metazoos, Chordata, Craniata, Glires; Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Rattus.

1 (Dases 1 to 783)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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     Matches:
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Pred. No.:

Score:

ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

DEFINITION

ACCESSION

RESULT 97 CK478920

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Search completed: March 17, 2006, 08:19:15 Job time : 3913 secs
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UI-M-FIO-byu-j-06-0-UI.rl NIH BMAP_FIO Mus musculus cDNA clone
IMAGE:5702501 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bopamatophyta, Bagnoliophyta, Liliopaida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.

1 (bases 1 to 809)
Mitcelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
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/note="vector: pGK4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 810)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
9712 Medical Center Drive, Rockville, MD 20850, USA
Fax: 901-838-0208
Email: whitelaw@tigr.org
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Mus musculus
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Unpublished (2003)
Other GSSs: PUFCY39TB
Contact: Cathy Whitelaw
genomic survey sequence.
BZ812231
BZ812231.1 GI:29024584
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/db xref="taxon:10090"
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/clone=lb="MINIE BMAP F10"
/clone=lb="MINIE BMAP F10"
/clone=lb="minie Wetcor: pYX- Asc; Site_l: EcoR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcs gel:First strand cDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACAC. This library was created for the University lows Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
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    .810
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="C57BL/6"

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GenCore Copyright (c) 1993

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Scoring table:

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US-09-989-890-238 212

Title: Perfect score:

Sequence:

March 17, 2006,

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OM protein

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Run

Total number of hits satisfying chosen

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Sequence 29003, A Sequence 1154, Ap Sequence 70, Appl Sequence 21077, A	Sequence 519, App Sequence 785, App	Sequence 16067, Sequence 598, Ap	Sequence 15, Apl Sequence 3448, 7	Sequence 2813, i Sequence 83, App	Sequence 6261, i	Sequence 2539, 7	Sequence 3448,	Sequence 332, A	Sequence 2447,	Sequence 3, App.	Sequence 5329,	Sequence 29663,	Sequence 2945/, Patent No. 51910	Sequence	Sequence 4515,	Sequence 6384, 7	Sequence 8692.	Sequence 13107,	Sequence 1232,	Sequence 7, App.	Sequence 2082, 1	Sequence 976, A	Sequence 976, A	Sequence 976, A	Sequence 976, Al	Sequence 976, A	Sequence 4215, 7	Sequence 2927, 1	Sequence 9, App.	Sequence 2052, Sequence 21483.	Sequence 3, App.	Sequence 3, App.	Sequence 3, App	Sequence 3, App.	Sequence 25678,	Sequence 28516,	Sequence 1612,	Sequence 7487,	Sequence 499, A	Sequence 5014,	Sequence 215, A	Sequence 215, A	Sequence 215, A	Sequence 215, A	Sequence 215, A	edneuce	equence	e c
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 05/041,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                              US-09-989-890-238 (1-212) x US-10-104-047-799 (1-1785)
                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                             Gaps:
                                                                                                   4.26e-95
115.00
99.1%
99.1%
54.2%
                TYPE: DNA
CORGANISM: Homo sapiens
US-10-104-047-799
                                                                                                                                        Percent Similarity:
Best Local Similarity:
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US-09-949-016-17032
                                                                                      Alignment Scores:
LENGTH: 1785
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                                                                                                                         Score:
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Sequence 12803, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 17032
LENGTH: 194937
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11.00
100.0%
100.0%
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17032
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US-09-949-016-17033
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; ORGANISM: Human
US-09-949-016-17033
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US-09-949-016-30921/C
; Sequence 30921, Application US/09949016
; Sequence 30921, Application US/09949016
; Patent No. 6812339
; GENERAL INPORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PLING DATE: 2000-10-20
; PRIOR PLING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTAME: PastSEQ for Windows Version 4.0
; SEQ ID NO 30921
LENGTH: 601
                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOL307
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARE: FRALESEQ for Windows Version 4.0
SEQ ID NO: 30920
LENGTH: 601
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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Best Local Similarity:
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ORGANISM: Human
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US-09-949-016-13967, Application US/09949016

Sequence 13967, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMOKPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SEC ID NO 13967

LENGTH: 31861
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEX ID NOS: 207012
SOFTWARE: FRSEESEQ for Windows Version 4.0
SEQ ID NO 12803
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US-09-949-016-30920/c
; Sequence 30920, Application US/09949016
; Patent No. 6812339
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10.00
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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; ORGANISM: Human
US-09-949-016-13967
                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
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Pred. No.:
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Pred. No.:
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US-09-949-016-30924/C

US-09-949-016-30924, Application US/09949016

Sequence 30924, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE FREENCE OF WINDOWS VERSION 4.0

SEQ ID NO 30924
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Sequence 168951, Application US/09949016

Patent No. 6812339

JEBERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-01-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESENCE OF Windows Version 4.0
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US-09-989-890-238 (1-212) x US-09-949-016-30923 (1-601)
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Matches:
Conservative:
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Matches:
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9.00
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Query Match:
DB:
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LENGTH: 601
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Pred. No.:
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j Sequence 30923, Application US/09949016

j Retent No. 681239

j GENERAL INFORMATION:

j APPLICANT: VENTER, J. Craig et al.

j TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

j FILE REPRENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

j PRIOR PLING DATE: 2000-10-03

pRIOR PLING DATE: 2000-10-03

j PRIOR PLING DATE: 2000-10-03

j PRIOR FILING DATE: 2000-10-03

j SOFTWARE: PSECIE NOWBER: 60/231,498

j NUMBER OF SECIE NOS: 207012

j SOFTWARE: PSECIE Windows Version 4.0

j SEQ ID NO 30923
                                                                                                                                                                                               ION AND USES THEREOF
                                                        US-9-99-1016-30222/C

Sequence 30922.2/C

Sequence 30922.2/C

Sequence 30922.2/C

Sequence 30922.2/C

Sequence 30922.2/C

Sequence 30922.2/C

SEGREAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND TITLE OF INVENTION WITHER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 601
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Human
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ORGANISM: Human
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Pred. No.:
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: uS/09/949, 016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 168954, Application US/09949016; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-168955/c; Sequence 168955, Application US/09949016; Patent No. 6812339
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; ORGANISM: Human
US-09-949-016-168954
     US-09-949-016-168953
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LENGTH: 601
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US-09-949-016-168952/C

i Sequence 168952, Application US/09949016

i Patent No. 6812339

i GENERAL INFORMATION:

i TITLE OF INVENTION: POLYMOKPHISMS IN KNOWN GENES ASSOCIATED

I TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

i PRIOR FILING DATE: 2000-10-03

i PRIOR FILING DATE: 2000-10-03

i PRIOR FILING DATE: 2000-10-03

i PRIOR SEQ ID NOS: 207012

i SOFTWARE: PSEAUSEQ for Windows Version 4.0

i LENGTH: 601
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GENERAL INFORMATION:
GENERAL INFORMATION:
FALLEN TO FUNDATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT PAPLICATION NUMBER: US/09/949,016
CURRENT PAPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PELLING DATE: 2000-10-03
PRIOR PELLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 168953
LENGTH: 601
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Mismatches:
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; Sequence 168953, Application US/09949016
; Patent No. 6812339
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Pred. No.:
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; SEQ ID NO 9034
; LENGTH: 1716
; TYPE: DNA
; CRGANISM: Myxococcus xanthus
US-09-902-540-9034
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Best Local Similarity:
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US-09-902-540-8319/C
i Sequence 8319, Application US/09902540
j Patent No. 683347
j GENERAL INFORMATION:
i APPLICANT: Goldman, Barry S.
i APPLICANT: Alale, Gregory J.
j APPLICANT: Slater, Steven C.
j APPLICANT: Wiegand, Roger C.
i TITLE OF INVERTION: Myxococcus xanthus Genome Sequences and Uses Thereof
j FILE REFERENCE: 38-10(15849)B
i CURRENT APPLICATION NUMBER: US/09/902,540
i CURRENT FILING DATE: 2001-07-10
j PRIOR PPLICATION NUMBER: 60/217,883
j RRIOR PLILING DATE: 2000-07-10
j NUMBER OF SEQ ID NOS: 16825
j SEQ ID NO 8319
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US-09-902-540-9034/c
; Sequence 9034, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Glater, Steven C.
; APPLICANT: Wiegand, Roger C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 168955
LENGTH: 601
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PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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; ORGANISM: Myxococcus xanthus
US-09-902-540-8319
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Query Match:
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Best Local Similarity:
                                                                            ORGANISM: Human
US-09-949-016-168955
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Pred. No.:
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Pred. No.:
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Sequence 21, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

TITLE OF INVENTION GENES: PA-0041 US

CURRENT PELING DATE: 2001-10-12

PRIOR PELING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program
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Patent No. 6727066
GENERAL INFORMATION:
GENERAL INFORMATION:
TIPLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919, 039
CURRENT FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-07-28
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                                                                        ; FEATURE:
; NAME/KEY: miso feature
; OTHER (NFORMATION: Incyte ID No. 6673545 2700132CB1
US-09-919-172-97
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; OTHER INFORMATION: Incyte ID No. 6673549 2700132CB1
US-09-976-594-21
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Matches:
Conservative:
Mismatches:
Indels:
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                LENGTH: 10432
TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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US-09-919-039-20/c
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Pred. No.:
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   SEQ ID NO 97
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US-09-940-016-15117/C

Sequence 15117, Application US/09949016

Sequence 15117, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: FOLYMONEPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMONEPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOL01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAESEQ for Windows Version 4.0

SEG ID NO 15117
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                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS; FILE REPERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172; CURRENT FILING DATE: 2001-07-30; PRIOR FILING DATE: 2000-07-28; NUMBER OF SEQ ID NOS: 102; SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                    7661 ACTCGAGGACCCCCCCCCCAACCCCTA 7635
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; LENGTH: 9198
TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-966
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9.00
100.0%
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9.00
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Human
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US-09-919-172-97/c
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Pred. No.:
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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US-09-949-016-16348
                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                       US-09-949-016-12410
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ORGANISM: Human
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Pred. No.:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PLILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOFTWARE: REBESEQ for Windows Version 4.0
: LENGTH: 16013
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| Sequence 12410, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CL001307
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                                                                                                                              NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. 6727066 2700132CB1
US-09-919-039-20
                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6812339
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NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
                                    SEQ ID NO 20
LENGTH: 10432
TYPE: DNA
ORGANISM: Homo Bapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-12988/c
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; ORGANISM: Human
US-09-949-016-12988
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US-09-949-016-16505/c

Sequence 16505, Application US/09949016

Sequence 16505, Application US/09949016

Sequence 16505, Application US/09949016

Sequence 16505, Application US/09949016

SEGUENCE OF THIS OF INVENTION: POLYMPRENENT IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR APPLICATION NUMBER: 60/241, 756

PRIOR APPLICATION NUMBER: 60/231, 768

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-0-04

PRIOR PRILNG DATE: 2000-0-0-08

SPRIOR PLILNG DATE: 2000-0-0-08

SPRIOR PLILNG DATE: 2000-0-0-08

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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Matches:
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12410
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Patent No. 6812339
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Best Local Similarity:
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RESULT 30

US-09-349-016-12345/c

i Sequence 12345, Application US/09949016

parent No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESGEERO FOR Windows Version 4.0
                                                Sequence 15642, Application US/09949016

Sequence 15642, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-14-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

LENGTH: 79634
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Matches:
Conservative:
Mismatches:
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US-09-949-016-12345
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LOCATION: (1)...(86414
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Best Local Similarity:
Query Match:
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; ORGANISM: Human
US-09-949-016-15642
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ORGANISM: Human
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1 Sequence 15318, Application US/09949016

1 Patcent No. 6812339

2 GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERRENCE: CL001307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: FBELSCE for Windows Version 4.0

LENGTH: 79595
           TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PELING DATE: 2000-10-20
FRIOR PILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 16348
LENGTH: 51252
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GENERAL INFORMATION:
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; ORGANISM: Human
US-09-949-016-15318
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ORGANISM: Human
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TILLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OP DETECTION AND USES THEREOF
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OP DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1)...(455726)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                  5.88e+03
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Best Local Similarity:
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ORGANISM: Human
                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12751
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      LENGTH: 148794
                                                                                                  Alignment Scores:
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JOS-193-99-106-15.758/Application US/09949016

JOSCH ABPLICANT: VENTER, Application US/09949016

JOSCH ABPLICANT: VENTER, APPLICATION:

JOSCH APPLICANT: VENTER, APPLICANTON: POLYMORHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOL307

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESE PRESEQ for Windows Version 4.0

SEQ ID NO 15758

LENGTH: 86414
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-04-14
PRIOR PLLING DATE: 2000-10-03
PRIOR PLLING DATE: 2000-10-03
PRIOR PLLING DATE: 2000-10-03
PRIOR PLLING DATE: 2000-09-08
PRIOR PLLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FaatSEQ for Windows Version 4.0
SEQ ID NO 12751
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Conservative:
Mismatches:
Indels:
Mismatches:
Indels:
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8-09-949-016-12751
; Sequence 12751, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LCCATION: (1)...(86414)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15758
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  Best Local Similarity: 100.0%
Query Match: 4.2%
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Query Match:
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US-09-949-016-15758/c
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Pred. No.:
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APPLICANT: Wohlgemuth, Jay,
APPLICANT: Wohlgemuth, Jay,
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE;
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT PILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-10-22
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFFWARE: Pacentin Version 3.1
SEQ ID NO 4540
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 96, Application US/08474633A
| Patent No. 5773691
| GENERAL INFORMATION:
| APPLICANT: E. I. DU PONT DE NEMOURS AND
| TITLE OF INVENTION: CHIMERIC GENES AND
| TITLE OF INVENTION: METHODS FOR INCREASING
| TITLE OF INVENTION: INCREASING THE LYSING
| TITLE OF INVENTION: OF THE SEEDS OF PLANTS
| NUMBER OF SEQUENCES: 107
| CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: FLORPY DISK
MEDIUM TYPE: FLORPY DISK
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
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ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ProSerSerLeuAlaLeuLeuSer 32
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                            Sequence 4540, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
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CITY: WILMINGTON
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Best Local Similarity:
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     JS-10-131-827-4540
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Pred. No.:
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DB:
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APPLICANT: Word and Code an
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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Indels:
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 69, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(481115)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-11940
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Alignment Scores:

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US-08-474-633A-97/C
; Sequence 97, Application US/08474633A
; Patent No. 5773691
; GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
TITLE OF INVENTION:
TITLE OF INVENTION: METHODS FOR INCREASING
TITLE OF INVENTION: INCREASING
TITLE OF INVENTION: INCREASING
TITLE OF INVENTION: AND THREONINE CONTENT
TITLE OF INVENTION: OF THE SEEDS OF PLANTS
CORRESPONDENCES: 107
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: E. I. DU PONT DE NEMOURS
STREET: 1007 MADPUM.
                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                  Length:
Matches:
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                               Gaps:
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CLASSIFICATION: 800
ATTORNEY, AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/POCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                  | TELEX: 8135420
| INFORMATION FOR SEQ ID NO: 96:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 55 base pairs
| TYPE: nucleic acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: DNA (genomic)
| US-08-474-633A-96
TELECOMMUNICATION INFORMATION TELEPHONE: 302-992-4931 TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
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STRANDEDNESS: single
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STATE: DELAWARE
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
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Sequence 20, Application US/08737524B

Sequence 20, Application US/08737524B

Seneral INFORMATION:
APPLICANT: CARL SAVERIO FALCO
APPLICANT: DOMINICK ANTHONY GUIDA, JR.
APPLICANT: MARX ELIZABETH HARNETT LOCKE
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS, CHIMERIC
TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
TITLE OF INVENTION: THE METHIONINE CONTENT OF THE SEEDS
TITLE OF INVENTION: OF PLANTS

NUMBER OF SEQUENCES: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: TALINGARY STATES OF AMERICA COUNTRY: DELAWARE COUNTRY: UNITED STATES OF AMERICA ZIP: 19898 COMPUTER: BOSKETTE: 3.50 INCH COMPUTER: IBM FC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS 95 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 (7.0) CURRENT APPLICATION NUMBER: US/08/737,5248 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1007 MARKET STREET
CITY: WILLINGTON
STAFF: AND COMPANY
STAFF: AND COMPANY
STAFF: AND COMPANY
Length:
Matches:
Conservative:
Mismatches:
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Conservative:
Mismatches:
                                                                                                                     US-09-989-890-238 (1-212) x US-08-474-633A-97 (1-55)
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                                                                      Indels:
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                                                                                    Gaps:
                                                                                                                                                       33 ArgProLeuSerProProAla 40
                                                                                                                                                                      49 CGCCCCTTAAGTCCACCGCCAGCC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 55 base pairs TYPE: nucleic acid
35.1
8.00
100.0%
100.0%
3.8%
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8.00
100.0%
100.0%
3.8%
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ADDRESSEE: E. I. DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
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                         Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                            US-08-737-524B-20
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Pred. No.:
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 Pred. No.:
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NUMBER OF SEQUENCES: 107
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Best Local Similarity:
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DB:
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                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: CARL SAVERIO FALCO
APPLICANT: CARL SAVERIO FALCO
APPLICANT: MAXY ELIZABETH HARNETT LOCKE
TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
TITLE OF INVENTION: GENES AND METHODS FOR INCREASING
TITLE OF INVENTION: THE METHICNINE CONTENT OF THE SEEDS
TITLE OF INVENTION: THE METHICNINE CONTENT OF THE SEEDS
TITLE OF INVENTION: THE METHICNINE CONTENT OF THE SEEDS
TITLE OF INVENTION: OF PLANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCES: 27
COUNTRY: UNIANGTON
STATE: DELAMARE
COUNTRY: UNIANGTON
STATE: DELAMARE
CONPUTER READBLE FORM:
MEDIUM TYPE: DISKETTE: 3.50 INCH
MEDIUM TYPE: DISKETTE: 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OMBERATION NUMBER: US/08/737,524B
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 30,971
REFERENCE LYNNE M. CHRISTENBUXY
REGISTRATION UNBER: 30,971
REFERENCE LOOKET NUMBER: 30,971
REFERENCE LOOKET NUMBER: 30,971
REFERENCE LOOKET NUMBER: 30,971
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMA
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 96, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
11 CGCCCCTTAAGTCCACCGCCAGCC 34
                                                           RESULT 40
US-08-737-524B-21/c
; Sequence 21, Application US/08737524B
; General INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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Pred. No.:
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US-08-823-771-96
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ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING INCREASING THE LYSINE AND THREONINE CONTENT
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-989-890-238 (1-212) x US-08-823-771-96 (1-55)
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CORRESPONDENCE ADDRESS: B. I. DU PONT DE NEMOURS
AND COMPANY
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 96:
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CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 CGCCCCTTAAGTCCACCGCCAGCC 34
                                                           STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-823-771-97/c
; Sequence 97, Application US/08823771
Patent No. 6459019
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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100.0%
3.8%
                                                                             CITY: WILMINGTON STATE: DELAWARE
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COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD VERSION 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,771
FILING DATE: 24-Mar-1997
CLASSIFICATION - UNKNOWN>
PRIOR APPLICATION ATA:
APPLICATION WUMBER: 08/474,633
FILING DATE: «Unknown>
ATTORNEY/AGENT INPORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,684
REFERRENCE/DOCKET NUMBER: 30,684
TELEGOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEGOMMUNICATION INPORMATION:
TELEGOMMUNICATION INPORMATION:
TELEBRAX: 302-972-4931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: E. I. DU PONT DE NEMOURS AND APPLICANT: COMPANY TITLE OF INVENTION: FRAGMENTS AND TITLE OF INVENTION: FRAGMENTS AND TITLE OF INVENTION: INCREASING THE STITLE OF INVENTION: LYSINE AND THREONINE TITLE OF INVENTION: CONTENT OF THE SEEDS TITLE OF INVENTION: OP PLANTS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
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MOLECULE TYPE: DNA (GELOMIC)

SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-823-771-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDLIW TYPE: DISKETTE, 3.50 INCH
COMPUTER: MACINTOSH
COMPUTER: MACINTOSH, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: B. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 ArgProLeuSerProProAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 CGCCCTTAAGTCCACCGCCAGCC 26
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                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 835420
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.1
8.00
100.0%
100.0%
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Best Local Similarity:
Query Match:
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Pred. No.:
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STATE: DE
COUNTRY:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PRAGRENTS AND TITLE OF INVENTION: PRAGRENTS AND TITLE OF INVENTION: PREHODS FOR TITLE OF INVENTION: LYSINE AND TITLE OF INVENTION: LYSINE AND THREOAINE TITLE OF INVENTION: CONTENT OF THE SEEDS NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: ADDRESSEE: ADD COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCREASING THE
LYSINE AND THREONINE
CONTENT OF THE SEEDS
OF PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US93-02480-20/c

Sequence 20, Application PC/TUS9302480
GENERAL INFORMATION:
APPLICANT: E. I. DU PONT DE NEMOURS AND
APPLICANT: COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02480
PILING DATE: 19930318
                                                                                                                                                                                    BB-1037-A
FILING DATE: 19930318
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,414
FILING DATE: 19 MARCH 1992
ATTORNEY/AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1037
TELEFONUNICATION INFORMATION:
TELEFONG 302-992-4929
TELEFONG: 302-992-4929
TELEFONG: 302-992-7949
TELEFON: 635420
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
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APPLICATION NUMBER: 07/855,414
FILING DATE: 19 WARCH 1992
ATTORNEY, AGENT INFORMATION:
NAME: LINDA AXAMETHY FLOYD
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic)
PCT-US93-02480-19
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: DELAWARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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Matches:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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FEBRUARIA INFORMATION:

GENUERAL INFORMATION:

GENUERAL INFORMATION:

FITLE OF INVENTION:

TITLE OF INVENTION:

THE SEEDS OF PLANTS

NUMBER OF SEQUENCES:

ADDRESSES:

ADDRESSES:

ADDRESSES:

CORRESPONDENCE ADDRESS:

ADDRESSES:

ADDRESSES:

CORRESPONDENCE ADDRESS:

ADDRESSES:

ADDRESSES:

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CONPUTRY:

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Matches:
Conservative:
Mismatches:
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REFERENCE/DOCKET NUMBER: BB-1037-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 ArgProLeuSerProProProAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 CGCCCCTTAAGTCCACCGCCAGCC 26
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ATTORNEY/ACENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30.684
REFERENCE/DOCKET NUMBER: BB-1;
TELEPOMONICATION INFORMATION:
TELEPHONE: 302-92-4931
TELEPHONE: 302-773-0164
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4929
TELEX: 302-892-7949
TELEX: 308-892-7949
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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TELEFAX: 835420
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 55 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
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8.00
100.0%
100.0%
3.8%
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Best Local Similarity:
Query Match:
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Pred. No.:
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ACT-USS9-08501-6/C

| Sequence 6, Application PC/TUS9508501
| GENERAL INFORMATION:
| APPLICANT: B. I. DU PONT DE NEMOURS AND COMPANY
| TITLE OF INVENTION: METHOD FOR INCREASING THE
| TITLE OF INVENTION: HE SEEDS OF PLANTS
| TITLE OF INVENTION: THE SEEDS OF PLANTS
| TITLE OF INVENTION: HE SEEDS OF PLANTS
| VUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS: ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY
| STREET: 1007 MARKET STREET
| CITY: WILMINGTON
| STATE: DELAWARE
| CONTRY: U.S.A.
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               Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19898
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: MIGROSOFT WORD
SOFTWARE: MIGROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 47
US-09-513-999C-12253/c
; Sequence 12253, Application US/09513999C
; Patent No. 6783961
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                                                                                                                                                                   11 CGCCCCTTAAGTCCACCGCCAGCC 34
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30.684
REFERENCE/DOCKET NUMBER: BB-1:
TELECHONIC CATION INFORMATION:
TELEPHONE: 302-92-4931
TELEFAK: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic) PCT-US95-08501-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 302-//-
TELEFAX: 35420
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
               100.0%
100.0%
3.8%
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STRANDEDNESS: single
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR PILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PATENTI VET: 2.0
SEG ID NO 97
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2217
LENGTH: 336
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                                                                   US-09-949-016-2217
; Sequence 2217, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 97, Application US/09123912A; Patent No. 6312695; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 cccrcagccrcagcagcaggr
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NAME/KEY: modified_base
LOCATION: (12)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified_base
LOCATION: (308)
OTHER INFORMATION: Where n is a, c,
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Human
US-09-949-016-2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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Pred. No.:
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Sequence 807, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ THARE: PSESEE FOR Windows Version 4.0

SEQ ID NO 807

LENGTH: 270
              APPLICANT: Duclert, A CHARLES FALLINE APPLICANT: Duclert, B CAMAILES, U. D. APPLICANT: Duclert, A CHARLES FALLINE APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
PRICE REPERENCE: 59. US2.REG
CURRENT APPLICATION NUMBER: US 609/513,999C
CURRENT PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 12533
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-989-890-238 (1-212) x US-09-513-999C-12253 (1-180)
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Conservative:
Mismatches:
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Mismatches:
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Dumas Milne Edwards, J.B.
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) LOCATION: 153

CTHER INFORMATION: r=a or g

US-09-513-999C-12253
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Best Local Similarity:
Query Match:
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Query Match:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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Pred. No.:
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Pred. No.:
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55 ProSerAlaSerAlaAlaGly 62

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LENGTH: 441
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210.11.4550.11
CURRENT APPLICATION NUMBER: 02/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 97
LENGTH: 441
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US-09-480-884A-97
Sequence 97, Application US/09480884A
Factor No. 6482597
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
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Matches:
Conservative:
Mismatches:
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     Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                      US-09-989-890-238 (1-212) x US-09-123-912-97 (1-441)
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                                                                                                                        55 ProSerAlaSerAlaAlaAlaGly 62
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Patent No. 6426072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature;
LOCATION: (1)...(441)
COTHER INFORMATION: n = A,T,C or G
US-09-643-597-97
                                                                                                                                                                                                                                                                                                           Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                   Wang, Aijun
Skeiky, Yasir A.W.
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8.00
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Fan, Liqun
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                             RESULT 51
US-09-643-597-97
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Panger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
FILE REPERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PASLESC for Windows Version 3.0
SEQ ID NO 97
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 97
LENGTH: 441
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US-09-606-421B-97
US-09-606-421B-97
, Sequence 97, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/09542615A Patent No. 6518256 GENERAL INFORMATION:
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| LOCATION: (1)...(441)

| OTHER INFORMATION: n = A,T,C or G

US-09-542-615A-97
                                                                                                                  NAME/KEY: misc_feature;
CCATION: (1)...(441)
UCHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
                                                                  TYPE: DNA
ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
DB:
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US-09-542-615A-97
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: LUNG CANCER;
FILE REPRENCE: 210121.455C5;
CURRENT APPLICATION NUMBER: US/09/476,496A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 97
LENGTH: 441
                                                                                                                                               Sequence 97, Application US/09466396A

Fatent No. 6696247

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REPERENCE: 210121.455C4

CURRENT PRILING DATE: 1999-12-17

CURRENT FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 224

SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
Conservative:
Mismatches:
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                 US-09-989-890-238 (1-212) x US-09-221-107-97 (1-441)
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; Patent No. 6706262
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US-09-466-396A-97
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NAME/KEY: misc_feature
LOCATION: (1)...(441)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
DB:
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US-09-466-396A-97
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Pred. No.:
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GENERAL INC. 8020530
GENERAL INCORNATION:
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REPERENCE: 210121.455C2
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PATENTIN VET. 2.0
                                                                                                               APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yaair A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PASTSEQ for Windows Version 3.0
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Patent No. 6660838
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OTHER INFORMATION: Where n is a,
                              Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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Wang, Tongtong
Fan, Ligun
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LOCATION: (308)
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LOCATION: (1)...(441)
OTHER INFORMATION: n =
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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US-09-221-107-97
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LENGTH: 441
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LENGTH: 441
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APPLICANT
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APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C10
CURRENT APPLICATION NUMBER: US/09/630,940B
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOFTWARE: FaetSEQ for Windows Version 3.0
LENGTH: 441
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Patent No. 6821518
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: LUNG CANCER
FILE REFERENCE: 210121.45562
CURRENT APPLICATION NUMBER: US/09/285,479
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 172
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 97
LENGTH: 441
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Conservative:
Mismatches:
Indels:
     Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                US-09-989-890-238 (1-212) x US-09-476-496A-97 (1-441)
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                                                                                                                                    ProSerAlaSerAlaAlaAlaGly 62
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                                                                                                                                                                                                                                        Sequence 97, Application US/09630940B Patent No. 6737514 GENERAL INFORMATION:
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LOCATION: (1)...(441)

JOTHER INFORMATION: n = A,T,C or G

US-09-630-940B-97
                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Panger, Nancy
APPLICANT: Panger, Gary R.
APPLICANT: Ii, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
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ORGANISM: Homo sapien
Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-630-940B-97
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Pred. No.:
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US-09-285-479-97
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APPLICANT: Cai, Feng
APPLICANT: Cai, Feng
APPLICANT: Poy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFRENCE: 210.21.45.5C.17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT PILLING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
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Patent No. 6560570
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Aijun
APPLICANT: Estelky, Yasir A.W.
APPLICANT: Li, Samual X.
APPLICANT: Kalos, Michael D.
CRGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(441)
COTHER INFORMATION: n = A,T,C or G
US-09-285-479-97
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LCCATION: 12, 308

CTHER INFORMATION: n = A,T,C or G

US-10-007-700-97
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McNeill, Patricia D.
Fanger, Neil
Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Peckman, David W.
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INPLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00790
CURRENT APPLICATION UNMER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
                                        TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 29,768
REFERENCE/POCKET NUMBER: 29,768
REFERENCE/POCKET NUMBER: 29,768
REFERENCE/POCKET NUMBER: 29,768
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
Indels:
                                                                                                                   ADDRESSEE: Folly & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STARE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 191, Application US/09949002
Patent No. 6900016
PARERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & L.
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Best Local Similarity:
Query Match:
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Retent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 21534

LENGTH: 479
                                                     US-09-270-767-6252

Sequence 6252, Application US/09270767

Sequence 6252, Application US/09270767

Sequence 6252, Application US/09270767

SERNBAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION:

FILE REFERENCE: FILE Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILLING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6252
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Matches:
Conservative:
Mismatches:
Indels:
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92 CCCTCAGCTTCAGCAGCAGGT 115
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Sequence 29, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster
US-09-270-767-6252
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Pred. No.:

RESULT 63

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Query Match: DB:

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Score:
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12-0891-789A-222
15-080-901-789A-222
15-080-901-780A-222
16-080-901-780A-222
17-080A-222
17-080A-222
18-080A-222
18-
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COUNTRY: USA

ZIP: 98104-7020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATE:
APPLICATION AUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: AUMBER: US/08/991,789A
ATTORINSY AGENT INFORMATION:
NAME: POTTER: Jane E. R.
REGISTRATION NUMBER: 33,332
REGISTRATION NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRHOME: (206) 682-6931
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 base pairs
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO: 222:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 191
LENGTH: 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 CTCCTCAGCAGGCCCTTGAGTCCC 401
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STATE: Washington
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Best Local Similarity:
Query Match:
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Query Match:
DB:
                                                                                                            TYPE: DNA
ORGANISM: Human
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Pred. No.:
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Sequence 222, Application US/09598326
Patent No. 6423496
GENERAL INFORMATION
APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Stewn G.
TITLE OF INFORTION COMPOSITIONS AND METHODS FOR THE
TITLE OF INFORTION TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                      APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPENDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STABET: Weahington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          578
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ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/062,451

FILING DATE: 04-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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153 TCGAGACCTCTGAGCCCACCTCCT 176
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                                                                                                 ; Sequence 222, Application US/09062451
; Patent No. 6344550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 247
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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100.0%
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Best Local Similarity:
Query Match:
                                                         RESULT 66
US-09-062-451-222
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US-09-598-326-222
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APPLICANT: Reed, Steven G
SEQ ID NO 222
LENGTH: 578
TYPE: DNA
CRGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(578)
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                              Pred. No.:
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APPLICANT: Migher, Lydda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 2101211.41952
CURRENT APPLICATION NUMBER: US/09/289,198
CURRENT FILING DATE: 1999-04-09
EARLIER PTLING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER APPLICATION NUMBER: US 08/991,762
EARLIER PILING DATE: 1997-04-09
EARLIER FILING DATE: 1997-04-09
EARLIER FILING DATE: 1997-01-0
EARLIER FILING DATE: 1997-01-0
EARLIER FILING DATE: 1996-08-20
EARLIER PILING DATE: 1996-08-20
EARLIER PILING DATE: 1996-08-20
EARLIER PILING DATE: 1996-08-20
EARLIER PILING DATE: 1996-01-01
           ADDRESSEE: Seed Intellectual Property Law Group PLLC STREET: 701 Fifth Avenue, Suite 6300
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPES FOR FORM:
MEDIUM TYPES FOR FORM:
MEDIUM TYPES FOR FORM:
MEDIUM TAPPLICATION DATA:
MAPPLICATION NUMBER: US/09/598,326
FILING DATE: 20-JUM-2000
CLASSIFTCATION:
ATTORNEY/AGENT INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                      NAME: Potter, Jane B.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 222: US-09-598-326-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 222:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 SerArgProLeuSerProProPro 39
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; Sequence 222, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
                                                     CITY: Seattle
STATE: Washington
COUNTRY: USA
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Best Local Similarity:
Query Match:
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Pred. No.:
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APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REPERENCE: 210121.419C
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
                                                                                                                                                         Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                              Length:
Matches:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 222
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Sequence 222, Application US/09429755A
; Patent No. 6656480
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-289-198-222
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; OTHER INFORMATION: n = A,T,C or G
US-09-429-755-222
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Smith, John M.
Reed, Steven G.
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.45521
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT PILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 98
         US-09-989-890-238 (1-212) x US-09-534-825A-222 (1-578)
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Matches:
Conservative:
Mismatches:
Indels:
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CTHER INFORMATION: Where n is a, c, g or US-09-123-912-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 CCCTCAGCTTCAGCAGCAGCAGGT 102
                                                                 32 SerArgProLeuSerProPro 39
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Fatent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Panger, Cattanya S.
APPLICANT: Panger, Cattanya S.
APPLICANT: Li, Samuel X.
                                                                                                                                        US-09-123-912-98
; Sequence 98, Application US/09123912A
; Patent No. 6312695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified_base
LOCATION: (285)
OTHER INFORMATION: Where n is a, c
NAME/KEY: modified_base
LOCATION: (349)
OTHER INFORMATION: Where n is a, c
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (489)
OTHER INFORMATION: Where n is a, NAME/KEY: modified base
LOCATION: (496)
OTHER INFORMATION: Where n is a, NAME/KEY: modified base
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Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-643-597-98
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APPLICANT:
APPLICANT:
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Patent No. 6861506

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Reid, Steven G.
APPLICANT: Reter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
FILE REFERENCE: 210121.419C7
CURRENT PAPLICANT: 2000-03-23
NUMBER OF SEQ ID NOS: 317
SOFTWARE: RettSEQ for Windows Version 3.0
APPLICANT: Migher, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C10
CURRENT FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 326
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 222
LENGTH: 578
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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LOCATION: (1)...(578)

CTHER INFORMATION: n = A,T,C or

US-09-534-825A-222
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8.00
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3.8%
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ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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US-09-534-825A-222
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Pred. No.:
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Pred. No.:
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SEQ ID NO 222
LENGTH: 578
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Fanger, Gary R.
Li, Samuel X.
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APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-606-421B-98
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LENGTH: 600
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 98
LENGTH: 600
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C6
                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-480-884A-98; Sequence 98, Application US/09480884A; Patent No. 6482597
                                                                                                                                                                                                                    NAME/KEY: misc_feature

LCCATION: (1)...(600)

CTHER INFORMATION: n = A,T,C or G

US-09-643-597-98
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US-09-480-884A-98
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100.0%
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3.8%
                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
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Query Match:
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Pred. No.:
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APPLICANT: Wang, Aijun APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERRNCE: 210121.45509
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
                                                                                                                   APPLICANT:
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Oary A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT PAPLICATION NUMBER: 2000-04-14
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 98
LENGTH: 600
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Mismatches:
Indels:
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Matches:
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SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 98, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 98, Application US/09606421B Patent No. 6531315 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // LOCATION: (1)...(600)
// OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-98
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Bangur, Chaltanya S.
Hosken, Nancy
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TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA .
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 1
Best Local Similarity: 1
Query Match: 3
DB:
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Best Local Similarity:
Query Match:
DB:
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Betent No. 6660838

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER FILE REFERENCE: 210121.455C2
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 98
LENGTH: 600
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Patent No. 6696247
GENERAL INFORMATION
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
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             Length:
Matches:
Conservative:
Mismatches:
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Conservative:
Mismatches:
Indels:
                                                                                                                 US-09-989-890-238 (1-212) x US-09-606-421B-98 (1-600)
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NAME/KEX: modified_base
NAME/KEX: modified_base
OTHER INFORMATION: Where n is a, c, g
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OTHER INFORMATION: Where n is a,
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NAME/KRY: modified_base
LOCATION: (489)
OTHER INFORMATION: Where n is
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LOCATION: (496)
OTHER INFORMATION: Where
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NAME/KEY: modified_base
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NAME/KEY: modified_base
LOCATION: (285)
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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US-09-466-396A-98
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Pred. No.:
 Alignment Scores:
Pred. No.:
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US-09-221-107-98
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GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Applicant: Hosken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: LING CANCER;
FILE REFRENCE: 210121.455C5
CURRENT APPLICATION NUMBER: US/09/476,496A
CURRENT PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 254
SOFTWARE: FASTERE for Windows Version 3.0
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Mismatches:
Indels:
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FILE REFERENCE: 210121.455C4
CURRENT APPLICATION NUMBER: US/09/466,396A
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 98
LENGTH: 600
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US-09-630-940B-98
; Sequence 98, Application US/09630940B
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; Sequence 98, Application US/09476496A
; Patent No. 6706262
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LOCATION: (600)

CTHER INFORMATION: n = A,T,C or G

US-09-466-396A-98
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US-09-476-496A-98
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APPLICANT: Cai, Feng
APPLICANT: Poy, Terega M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 210.21.455.01.
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
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Conservative:
Mismatches:
Indels:
US-09-989-890-238 (1-212) x US-09-285-479-98 (1-600)
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
LENGTH: 600
                                                             79 cccrcagcrrcagcagcaggr 102
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                                                                                                                            Sequence 98, Application US/10007700; Patent No. 6960570; GENERAL INFORMATION:
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; LOCATION: 295, 349, 489, 496, 583
; OTHER INFORMATION: n = A,T,C or G
US-10-007-700-98
                                                                                                                                                                                                                                          Kalos, Michael D.
Henderson, Robert A.
McNeill, Patricia D.
Fanger, Neil
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Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
Watanabe, Yoshihiro
Peckman, David W.
                                                                                                                                                                             APPLICANT: Wang, Tongtong
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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US-10-007-700-98
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                                                                                                                                    APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPRENCE: 210121,455C10
CURRENT APPLICATION NUMBER: US/09/630,940B
CURRENT RILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 98
LENGTH: 600
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; Sequence 98, Application US/09285479
; Patent No. 6821518
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; TITLE OP INVENTION: LUNG CANCER;
; FILE REPERENCE: 210.21.455.23
; CURRENT APPLICATION NUMBER: US/09/285,479
; CURRENT PILING DATE: 1999-04-02
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 98
; LENTH: 600
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LOCATION: (1)...(600)
OTHER INFORMATION: n = A,T,C or G
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LCCATION: (1)...(600)

JOTHER INFORMATION: n = A,T,C or G

US-09-285-479-98
                            Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
                                                                                                                              Skeiky, Yasir A.W
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 : Wang, Tongtong
: Fan, Liqun
                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-285-479-98
                                                             APPLICANT:
APPLICANT:
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APPLICANT:
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DS-95949-U6-38879, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
                     FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 33.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38879
LENGTH: 601
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-949-016-33707
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US-09-949-016-72530
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Pred. No.:
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Facett No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILLE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

FRIOR PILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

FRIOR FILING DATE: 2000-09-08

FRIOR FILING DATE: 2000-09-08

SPRIOR PILING DATE: 2000
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.;
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25331
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-30352
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; ORGANISM: Human
US-09-949-016-25231
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US-09-949-016-33707
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ORGANISM: Human
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Pred. No.:
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Pred. No.:
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JOSTON 1943-1010-1843/

Sequence 88437, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLOOM 1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: PSELSEE FORESEE FO
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Sequence 92611, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

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102 CCCTCAGCCTCAGCAGCAGGT 125
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Best Local Similarity:
Query Match:
                                                                                              RESULT 89
US-09-949-016-88437
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ORGANISM: Human
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LENGTH: 601
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Pred. No.:
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Sequence 76311, Application US/09949016

Sequence 76311, Application US/09949016

Sequence 76311, Application US/09949016

Sequence 76311, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 76311
                                                                              JAPELICATION STATES, J. Craig et al.

APPLICATE: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FaetSEQ for Windows Version 4.0

LENGTH: 601
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Matches:
Conservative:
Mismatches:
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Sequence 72530, Application US/09949016
Patent No. 6812339
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Best Local Similarity:
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US-09-949-016-72530
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; ORGANISM: Human
US-09-949-016-76311
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US-09-949-016-133788/c

US-09-949-016-133788/c

Sequence 133788 Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

PAPLICATY: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-109-08

NUMBER OF SECIED NOS: 207012

SOFTWARE: FastERQ for Windows Version 4.0

SEQ ID NO 133788
                                                                                                                                                                                                                                                                                                                US-09-949-016-123793

15 Sequence 123793, Application US/09949016

17 Sequence 123793, Application US/09949016

18 Patent No. 6812339

18 GENERAL INPORMARION:

19 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

18 TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

18 TILE REFERENCE CLO01307

19 TILE REFERENCE CLO01307

10 CURRENT APPLICATION NUMBER: US/09/949,016

10 CURRENT FILING DATE: 2000-04-14

10 PRIOR APPLICATION NUMBER: 60/237,768

11 PRIOR FILING DATE: 2000-10-20

12 PRIOR FILING DATE: 2000-10-03

13 PRIOR FILING DATE: 2000-09-08

14 NUMBER OF SEQ ID NOS: 207012

15 SOFTWARE: FREASEQ for Windows Version 4.0

16 SEQ ID NO 123793

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Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ORGANISM: Human
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Sequence 92612, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENENT: COLO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 92612

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SEQ ID NO 92612
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Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR PILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: PEASESEQ for Windows Version 4.0

LENGTH: 601

LENGTH: 601
                                              US-09-989-890-238 (1-212) x US-09-949-016-92611 (1-601)
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Matches:
Conservative:
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US-09-949-016-92612
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ORGANISM: Human
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US-09-949-016-92613
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ORGANISM: Human
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Alignment Scores:

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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTHANE: PSESESE for Windows Version 4.0
SEQ ID NO 141155
LENGTH: 601
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01204
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 141154
LENGTH: 601
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; Sequence 141155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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ORGANISM: Human
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ORGANISM: Human
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Sequence 13789, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/24,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESEQ for Windows Version 4.0

SEQ ID NO 133789
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US-09-949-016-141154
is Sequence 141154
pt 16153, Application US/09949016
pt Patent No. 681239
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Query Match:
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US-09-949-016-133789/c
  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-133788
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; ORGANISM: Human
US-09-949-016-133789
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US-09-949-016-147591

Sequence 147591, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VERTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 147591

LENGTH: 601
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FLING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-8
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 147427
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Sequence 157906, Application US/09949016

PARCEL NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
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ORGANISM: Human
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ORGANISM: Human
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Sequence 2002, Ap Sequence 143483, Sequence 143484, Sequence 143484, Sequence 143483, Sequence 143484, Sequence 134, App Sequence 134, App Sequence 52, Appl

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Sequence 760, App Sequence 20857, A Sequence 1, Appli Sequence 6100, Ap

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3937, App 73, App 73, App 173, App 173, App 488, App 84925, A

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US-10-156-761-411

US-09-919-172-97

US-09-919-039-20

US-10-133-1349

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-MODEL=frame+_D2n.model -DEV=xlh
-MODEL=frame+_D2n.model -DEV=xlh
-Col_Abbs_KBSEWEB spool/10509998990/runat_16032006_095520_17643/app_query.fasta_1
-DB=Published_App_ications_NA_Main -OFWT=fastap -SUFFIX=01igo_p2n.mpbm
-MINMATCH=0.1_-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01igo
-MINMATCH=0.1_-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -NATRIX=01igo
-ALIGN=100 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -HOST=abss03h
-NAXIEN=2000000000 -HOST=abss03h
-NO MAAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-NO MAAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -KGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
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Sequence 799, App
Sequence 12051, A
Sequence 124, App
Sequence 56, Appl
Sequence 517, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 GCCTGCTCTGGCGACCCTGGGTGTGGTGCCGGGCTGCCTTCTGCTTCCGCCGCT
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TITLE OF INVENTION: No. US20030236392A1el full length cDNA
FILE REFERENCE: H1-A0105
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                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,509
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin version 3.1
SEQ ID NO 105
LENGTH: 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 799, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
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                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-890-105
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Best Local Similarity:
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US-10-104-047-799
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OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE
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Matches:
Conservative:
Mismatches:
Indels:
             CURRENT APPLICATION NUMBER: US/10/779,543
CURRENT FILING DATE: 2004-02-12
CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 10/076,555
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 1993-12-21
PRIOR FILING DATE: 1993-12-21
PRIOR FILING DATE: 1997-12-23
PRIOR FILING DATE: 1996-04-03
PRIOR FILING DATE: 1996-04-03
PRIOR PILING DATE: 1996-04-03
PRIOR PILING DATE: 1996-04-03
PRIOR PILING DATE: 1996-04-03
PRIOR PILING DATE: 1996-02-12
PRIOR PILING DATE: 1996-00-12
PRIOR PILING DATE: 1996-00-12
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1998-02-24
PRIOR PILING DATE: 1998-02-24
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PRIOR PILING DATE: 1998-03-31
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US-10-779-543-12051
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ORGANISM: Homo sapiens
FEATURE:
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Pred. No.:
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APPLICANT: Macina, Roberto
APPLICANT: Macina, Herve
APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
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                                                                                                                   TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific TITLE OF INVENTION: Genes and Proteins FILE REFERENCE: DEX-0313
CURRENT APPLICATION NUMBER: US/10/074,475
CURRENT FILING DATE: 2002-02.13
PRIOR APPLICATION NUMBER: 60/268,292
PRIOR FILING DATE: 2001-02-13
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 CCCCCCAGCCCTGATCGTG 333
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Hu, Ping
Recipon, Herve
Karra, Kalpana
Cafferky, Robert
Sun, Yongming
Liu, Chenghua
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SOFTWARE: Patentin version
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US-10-074-475-124
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Best Local Similarity:
Query Match:
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Pred. No.:
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LENGTH: 654
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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477 GCCTGCTCTGGCGACCCTGGGTGTGGGAGTGGTGCCGGGCTGCCTTCTGCTTCCGCC 533
                                   RESULT 7

US-10-741-601-5611

US-10-741-601-5611

Sequence 5611, Application US/10741601

Publication No. US20040166519A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLO01500

CURRENT APPLICATION UNMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFFMARE: PRESENCE for Windows Version 4.0
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| Publication No. US20020182586A1
| GENERAL INPORMATION:
| APPLICANT: Engelhard, Eric K.
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
| TITLE OF INVENTION: OGNICE
| FILE REFERENCE: 529452000122
| CURRENT APPLICATION NUMBER: US,10/087,192
| CURRENT FILING DATE: 2000-12-22
| PRIOR APPLICATION NUMBER: US 09/747,377
| PRIOR PRILING DATE: 2000-12-22
| PRIOR FILING DATE: 2001-03-02
| NUMBER OF SEQ ID NOS: 2059
| SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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US-10-087-192-2002
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 253861
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LENGTH: 261817
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APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REPERENCE: DEX-0291
CURRENT PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 66/252,500
PRIOR APPLICATION NUMBER: 66/252,500
WUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416
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Patent No. US20020172957A1
GENERAL INFORMATION:
; SOFTWARE: PatentIn version 3.1; SEQ 1D NO 56; LENGTH: 1977
; TYPE: DNA; TYPE: DNA
; ORGANICM: Homo sapien
US-09-989-920-56
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APPLICANT: Recipon, Herve
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; ORGANISM: Homo sapien
US-09-989-920-117
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Best Local Similarity:
Query Match:
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LENGTH: 1977
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 143484 LENGTH: 523 TYPE: DNA ORGANISM: Human
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Sequence 143483, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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US-10-027-632-143484
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US-10-027-632-143483
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Pred. No.:
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                 US-10-027-632-143483

US-10-027-632-143483

Sequence 143483, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Inductification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,318

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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| Sequence 143484, Application US/10027632
| Publication No. US20020198371A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G. |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| FILE REFERENCE: 108627.129 |
| CURRENT APPLICATION NUMBER: US/10/027,632 |
| CURRENT APPLICATION NUMBER: US 60/218,006 |
| PRIOR APPLICATION NUMBER: US 60/198,676 |
| PRIOR APPLICATION NUMBER: US 60/198,676 |
| PRIOR FILING DATE: 2000-04-20 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 1999-11-23 |
| PRIOR PILING DATE: 1999-09-28 |
| PRIOR PILING DATE: 1999-09-28 |
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 143483
LENCTH: 523
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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US-10-027-632-143484
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US-10-027-632-143483
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GAPPLICANT: Wang, David G.

TITLE OF INVENTION: Tedentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-24
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PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-108-28
PRIOR PLING DATE: 1999-108-28
PRIOR PLING DATE: 1999-10-24
PRIOR PLING DATE: 1999-108-28
PRIOR PLING DATE: 1999-108-38
PRIOR PLING DATE: 1999-108-38
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-08
PRIOR PLING DATE: 1999-08-09
PRIOR PLING DATE: 1999-08-08
PRIOR PRIOR DATE: 19
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PILING DATE: 2002-04-30
RIOR APPLICATION NUMBER: US 60/196,006
PRIOR APPLICATION NUMBER: US 60/196,006
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
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Mismatches:
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIKAWA, HROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 4893
LENGTH: 861
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LENGTH: 523
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US-10-156-761-4893
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NAME/KEY: CDS
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Pred. No.:
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Alignment Scores:

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APPLICANT: HULGATTE, REMICLES
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUTEN, CATHERINE
APPLICANT: NGUTEN, CATHERINE
APPLICANT: NGUTEN, CATHERINE
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT APPLICATION NUMBER: 60/254,090
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE PREENT NOT: 2.1
SEQ ID NO 134
LENGTH: 5723
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Publication No. US20030215835A1
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REPRENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: US 60/348,164
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR PILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: forkhead box ola (rhabdomyosarcoma) (FOXOIA); OTHER INFORMATION: gene.
US-10-007-926A-134
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                                                                                                                                                      US-09-989-890-238 (1-212) x US-10-156-761-4893 (1-861)
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Matches:
Conservative:
Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                  51 GlyAlaGlyLeuProSerAlaSerAlaAla 60
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                                                                                                                                                                                                                                                                                                                       Sequence 134, Application US/10007926A Publication No. US20030143539A1 GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin version 3.1
SEQ ID NO 52
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ORGANISM: Homo sapiens
                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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DB:
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FEATURE:
NAME/KEY: SIMILAR
LOCATION: (1585)
OTHER INFORMATION: 31% homologous to Homo sapiens fork head domain
OTHER INFORMATION: protein, accession number U02310, Smith-Waterman Score=53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CH39/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR FILING DATE: 2003-06-11
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 20857
LENGTH: 5833
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT PEPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Petentin version 3.2
SEQ ID NO 760
LENGTH: 5723
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-450-763-20857
Sequence 20857, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
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US-10-156-761-1/c
Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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US-10-956-157-760
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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                                                                                                                          TYPE: DNA
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US-10-956-157-760

US-10-956-157-760

Squence 760, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William

TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10671074

Sequence 10 VIS20040097459A1

GENERAL INFORMATION:

APPLICANT: Debie, Kenneth W.

APPLICANT: Bhanot, Sanjay

APPLICANT: Veniant-Ellison, Murielle

APPLICANT: Veniant-Ellison, Murielle

APPLICANT: Shutter, John R.

TILLE OF INVENTION: MODULATION OF FORKHEAD BOX OIA EXPRESSION

FILE REFERENCE: AMGNOOL-101

CURRENT APPLICATION NUMBER: US/10/671,074

CURRENT FILING DATE: 2003-09-25

PRIOR FILING DATE: 2002-09-26
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Matches:
Conservative:
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Mismatches:
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Gaps:
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SEQ ID NO 4
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; LOCATION: (386)...(2353)
US-10-671-074-4
                                                                   ; NAME/KEY: CDS
; LOCATION: (386)..(2350)
; OTHER INFORMATION:
US-10-341-434-52
                  TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: H. sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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   LENGTH: 5723
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Sequence 6190, Application US/10719993

Fublication No. US20040265849A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
ALZHEIMERFENCE: CLO01496

FILE REPERENCE: CLO01496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55542

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 201
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Publication No. US20040265849A1
Publication No. US20040265849A1
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISRASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERBINCE: CLO01496
CURRENT APPLICATION NUMBER: US/10/719,993
NUMBER OF SEC ID NOS: 55342
SOFTWARE: FREESEQ FOR WINDOWS Version 4.0
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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Matches:
Conservative:
Mismatches:
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; Publication No. US20040265849A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-719-993-6190
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CORGANISM: Homo sapiens
US-10-719-993-6280
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-719-993-6280/c
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LENGTH: 201
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Publication No. US20040265849A1
GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: GREETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6100
LENGTH: 201
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Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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  APPLICANT: ISHIRAMA, JUNA
APPLICANT: ISHIRAMA, HIROSHI
APPLICANT: HORIKAMA, HIROSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: HATYORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2002-05-29
PRIOR PLLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PLLING DATE: 2001-06-30
PRIOR PLLING DATE: 2001-06-30
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
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; ORGANISM: Homo sapiens
US-10-719-993-6100
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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LENGTH: 9025608
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                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CLOO1496
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARER FREESEQ for Windows Version 4.0
SEQ ID NO 6416
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3971, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GARGILON SOLVENCE OF DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1496
CURRENT APPLICATION NUMBER: US/10/719, 993
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FREESEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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Mismatches:
Indels:
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Publication No. US20030224379A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Xonghong
APPLICANT: Weng, Zonghong
APPLICANT: Weng, Zonghong
APPLICANT: Weng, Zonghong
APPLICANT: Weng, Zonghong
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 807A
                                                                                                                                                                                                                                                                                                                                                                                                         172 GCTCTTCTTTCACGCCCACTTTCCCCA 146
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; ORGANISM: Homo sapiens
US-10-719-993-6416
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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US-10-719-993-39711/c
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US-10-243-552-741/c
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LENGTH: 201
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Pred. No.:
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CURRENT APPLICATION NUMBER: US/10/243,552

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LOCATION: (151)...(237)
CTHER INFORMATION: 75% homologous to Homo sapiens BB1=malignant cell expression-OTHER INFORMATION: enhanced gene/fumor progression-enhanced gene, accession number;
CTHER INFORMATION: S82470, Smith-Waterman Score=116.
PRIOR PELLING DATE: 2002-09-12
PRIOR PELLING DATE: 2001-09-13
PRIOR PELLING DATE: 2001-09-13
PRIOR PELLING DATE: 2001-09-13
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-01-21
PRIOR PELLING DATE: 2000-01-21
PRIOR PELLING DATE: 2000-01-21
PRIOR PELLING DATE: 2000-01-25
PRIOR PELLING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/USO1/02623
PRIOR PELLING DATE: 2001-01-25
PRIOR PELLING DATE: 2000-01-25
PRIOR PELLING DATE: 2000-01-25
PRIOR PELLING DATE: 2000-01-25
PRIOR PELLING DATE: 2000-01-26
PRIOR PELLING DATE: 2000-01-26
PRIOR PELLING DATE: 2000-01-26
PRIOR PELLING DATE: 2000-01-26
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2001-02-26
PRIOR PELLING DATE: 2000-04-27
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FILLE REPERENCE: 790(TP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: OT/US01/08631
PRIOR PLING DATE: 2001-03-30
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CLASTOM
SEQ TO NO 10524
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Matches:
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-243-552-741
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ORGANISM: Homo sapiens
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Gaps:

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Sequence 73, Application US/10799747
Publication No. US20040157258A1
GENERAL INFORMATION:
JAPPLICATE: ROSEN et. al
TITLE OF INVENTION: 101 Human Secreted Proteins
FILE REPRENCE: PS017P1
CURRENT APPLICATION NUMBER: US/10/799,747
CURRENT FILING DATE: 2004-03-15
PRIOR APPLICATION NUMBER: US/09/281,976
PRIOR APPLICATION NUMBER: US/09/281,976
PRIOR PELING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/060,837
PRIOR FILING DATE: 1997-10-02
PRIOR PRIOR PRIOR DATE: 1997-10-02
PRIOR PRIOR PRIOR DATE: 1997-10-02
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TITLE OF INVENTION: 101 Human Secreted Proteins
FILE REFERENCE: P2017P1
CURRENT APPLICATION NUMBER: US/10/979,183
CURRENT FILING DATE: 2004-11-03
FRICR APPLICATION NUMBER: US/10/799,747
PRICR APPLICATION NUMBER: US/10/199,730
PRICR APPLICATION NUMBER: US/10/195,730
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US-10-979-183-73/C
is Sequence 73, Application US/10979183
Publication No. US20050069943A1
GENERAL INFORMATION:
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                  TYPE: DNA
CORGANISM: Homo sapiens
US-10-195-730-73
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CORGANISM: Homo sapiens
US-10-799-747-73
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LENGTH: 546
LENGTH: 546
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
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                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Publication No. US20030144492A1

GENERAL INFORMATION:

APPLICANT: ROSEN et. al

TITLE OF INVENTION: 101 Human Secreted Proteins
FILE REFERENCE: PZ017P1

CURRENT APPLICATION NUMBER: US/10/195,730

CURRENT APPLICATION NUMBER: US/09/281,976

PRIOR PRING DATE: 1999-03-31

PRIOR FILING DATE: 1999-10-02

PRIOR PLILING DATE: 1997-10-02

SEQ ID NO 73
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Matches:
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 3937
LENGTH: 496
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Publication No. US20030073623A1
GENERAL INFORMATION:
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; LOCATION: (1)...(496)
; OTHER INFORMATION: n =
US-09-918-995-3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-918-995-3937/c
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US-10-195-730-73/c
                  Alignment Scores:
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US-09-764-815-478
US-09-764-815-478

| Sequence 478, Application US/09764875
| Publication No. US20040018969A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: NUMBER: US/09/764,875
| CURRENT FILING DATE: 2001-01-17
| Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1249
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 488, Application US/10264237; Publication No. US20040009491A1; GENERAL INFORMATION:
APPLICANT: Birse et al., TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PA131P1
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Matches:
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PRIOR APPLICATION NUMBER: US/09/281,976
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: 60/060,837
PRIOR PILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 390
SOFTWARE: PATCHIN VGT: 2.0
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COCATION: (34)
I. OTHER INFORMATION: n equals a,t,g, or c
US-09-764-875-478
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; ORGANISM: Homo sapiens
US-10-979-183-73
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Best Local Similarity:
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US-10-264-237-488
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Www. Wei
APPLICANT: Www. Wei
APPLICANT: Baubazuk, Brad
APPLICANT: Baubazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT PILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
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Conservative:
Mismatches:
Indels:
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US-10-437-963-84925
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CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR PILING DATE: 2001-05-18
PRIOR PILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver: 3.1
SEQ ID NO 488
LENGTH: 562
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LOCATION: (34)...(34)
OTHER INFORMATION: n equals a,t,g, or
FRATURE:
LOCATION: (473)...(473)
OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (480)

COTHER INFORMATION: n equals a,t,g, or

US-10-264-237-488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 84925, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.4
9.00
100.0%
100.0%
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9.00
100.0%
100.0%
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ORGANISM: Oryza sativa
                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-10-437-963-84925/c
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Pred. No.:
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Sequence 726141, Application US/09925065A

Sequence 726141, Application US/09925065A

Publication No. US2005028172A9

GENERAL INFORMATION:

APPLICATY: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

PILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/260,092

PRIOR APPLICATION NUMBER: US 60/260,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-989-890-238 (1-212) x US-09-925-065A-726141 (1-652)
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Matches:
Conservative:
Mismatches:
                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
; ORGANISM: Oryza sativa
; FEATURE:
DTHER INFORMATION: Clone ID: PAT_MRT4530_20732C.1
US-10-437-963-14833
                                                                                                                                                                                                                                                                          Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 LeuAlaLeuLeuSerArgProLeuSer 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Budworth, Paul R. APPLICANT: Moughamer, Todd G. APPLICANT: Briggs, Steven P. APPLICANT: Cooper, Bret APPLICANT: Glazebrook, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glazebrook, Jane
Goff, Stephen A.
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9.00
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Best Local Similarity:
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Best Local Similarity:
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US-10-260-238-4042/c
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DB:
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; Sequence 14833, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Brabauk, Brad
    APPLICANT: Brabauk, Brad
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants (153221) B
    CURRENT APPLICATION NUMBER: US/10/437,963
    CURRENT FILING DATE: 2003-05-14
    NUMBER OF SEQ ID NOS: 204966
    SEQ ID NO 14833
    LENGTH: 645
                                                                                                                                                                                                                                                                                                                                  GENERAL INFURMATION:

GENERAL INFURMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR SPOILON NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957066
SOFTWARE: FRAEESEQ FOR Windows Wersion 4.0
SEQ ID NO 468689
LENGTH: 637
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                             33 ArgProLeuSerProProProAlaAla 41
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                                                                                                                                                                                                                                                                  Sequence 468689, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
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100.0%
4.2%
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US-09-925-065A-468689
                                                                                                                                                                                                                  RESULT 34
US-09-925-065A-468689/c
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Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence_280, Application US/10296115

Publication No. US20040053248A1

GENERAL INFORMATION:

APPLICANT: Hyeed Inc.

TITLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 784PCT

CURRENT APPLICATION NUMBER: US/10/296,115

CURRENT APPLICATION NUMBER: US/9488,725

PRIOR APPLICATION NUMBER: US/9488,725

PRIOR PELING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478
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APPLICANT: COOPEY, Bret.
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: BLOWENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE OF INVENTION NUMBER: US 60/325,448
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-46
                                                                                                                    US-09-989-890-238 (1-212) x US-10-260-238-4040 (1-737)
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Best Local Similarity: 100.0%
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9.00
100.0%
100.0%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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               APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 6011.NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-6
PRIOR FILING DATE: 2001-04-6
PRIOR FILING DATE: 2001-04-6
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 4042
LENGTH: 717
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
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Katagiri, Fumiyaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-260-238-4042
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9.00
100.0%
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9.00
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Query Match:
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Pred. No.:
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Pred. No.:
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WESULF 43

US 10-087-080-31/c

Sequence 31, Application US/10087080

Publication No. US20030235820A1

GENERAL INFORMATION:

APPLICANT: Mark, David H.

APPLICANT: Bos Biotechnology, Inc.

APPLICANT: Case Western Reserve University

TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for

TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for

TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for

TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for

TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for

TITLE REPERBENCE: 018501-0004400S

CURRENT APPLICATION NUMBER: US 60/272,206

PRIOR APPLICATION NUMBER: US 60/272,206

PRIOR APPLICATION NUMBER: US 60/281,149

PRIOR PILING DATE: 2001-04-17

PRIOR PILING DATE: 2001-04-17

SEQ ID NO 31

LENGTH: 1209

LENGTH: 1209

LENGTH: 1209
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION WUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 34733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: winged helix/forkhead transcription factor (HFH1)
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                            , OTHER INFORMATION: Clone ID: PAT_MRT4530_3871C.1 US-10-437-963-34733
                                                                                                                                                                                                                                                                                      Length:
Matches:
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OTHER INFORMATION: n = g, a,
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                                                                                                                                                     TYPE: DNA
ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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APPLICANT: LA CANALIGATION:
APPLICANT: Enou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Broukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)21)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 86193
LENGTH: 891
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                                                                                                             Length:
Matches:
Conservative:
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Matches:
Conservative:
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US-10-437-963-86193
                                                                                                                                                                                                                                                                                                            455 CTGCCTTCTTCATTGGCGCTGTTGTCG 429
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Baubazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 86193, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                 TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-260-238-4041
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ORGANISM: Oryza sativa
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Best Local Similarity:
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Pred. No.:
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Sequence 9, Application US/10274177;
Publication No. US20040038225A1
GENERAL INFORMATION:
GENERAL INFORMATION:
JITLE OF INVENTION: METHODS FOR CATECORIZING PATIENTS
FILE REFREENCE: CWRU-PO1-003
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US/10/274,177
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US/10/229,345
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
FILING DATE: 2002-08-26
SOFTWARE: Patentin version 3.1
                                                                                               Sequence 9, Application US/10229345
Publication No. US20040038220A1
GENERAL INFORMATION:
APPLICANT: MARKOWITZ, Sanford D.
TITLE OF INVENTION: METHODS FOR CATEGORIZING PATIENTS
FILE REFERENCE: CWRU-P01-003
CURRENT APPLICATION NUMBER: US/10/229,345
CURRENT FILIG DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
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Matches:
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                  242 GCTGCTGCCGGATCGCCTCCTCCGCG 216
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NAME/KEY: misc feature
LOCATION: (1161)..(1161)

OTHER INFORMATION: n=a, c, g, or t
US-10-274-177-9
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; LOCATION: (1161)..(1161)
OTHER INFORMATION: n=a, c, g, or t
US-10-229-345-9
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-274-177-9/c
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Pred. No.:
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Pred. No.:
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RESULT 46

US-10-650-112-9/C

J Sequence 9, Application US/10650112

Publication No. US20040110712A1

GENERAL INFORMATION:

APPLICANT: WARKOWITZ, Sanford D.

TILLE OF INVENTION: WHENCY INTEATING PATIENTS AND IDENTIFYING THERAPEUTICS

PILE REFERENCE: CWRU-P01-044

CURRENT APPLICATION NUMBER: US/10/650,112

CURRENT PAIL OF TILLING DATE: 2002-10-18

PRIOR PILLING DATE: 2002-10-18

PRIOR PLILING DATE: 2002-10-18

PRIOR PLILING DATE: 2002-08-26

PRIOR PLILING DATE: 2002-08-26

PRIOR PLILING DATE: 2002-08-26

PRIOR PLILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 27

FEMALE. PATENTING DATE: 2002-08-27

SOFTWARE: Patentin version 3.2
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US-11-041-788-9/C
Sequence 9, Application US/11041788
Publication No. US20050233353A1
GENERAL INFORMATION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR FILE REFERENCE: CWRU-P04-003
CURRENT APPLICATION NUMBER: US/11/041,788
CURRENT APPLICATION NUMBER: US 10/649,591
PRIOR FILING DATE: 2003-08-26
PRIOR PILING DATE: 2003-08-26
PRIOR PELING DATE: 2002-02-27
PRIOR FILING DATE: 2002-02-27
PRIOR FILING DATE: 2002-02-27
PRIOR FILING DATE: 2001-04-17
PRIOR PELING DATE: 2001-04-17
PRIOR PELING DATE: 2001-04-17
PRIOR PELING DATE: 2001-04-17
PRIOR PELING DATE: 2001-04-07
PRIOR PELING DATE: 2001-04-07
PRIOR PELING DATE: 2001-04-07
PRIOR PELING DATE: 2001-04-07
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PRIOR PELING DATE: 2001-04-02
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                              242 GCTGCTGCCGGGATCGCCTCCTCCGCG 216
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59 AlaAlaAlaGlyIleAlaSerSerAla 67
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NAME/KEY: misc feature

LOCATION: (1161)..(1161)

OTHER INFORMATION: n is a,t,g or c
US-10-650-112-9
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Best Local Similarity:
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Sequence 1, Application US/10471010
Publication No. US20040185527A1
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CL001044-US
CURRENT APPLICATION UNMERR: US/10/471,010
CURRENT FILING DATE: 2003-09-08
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Fublication No. US20040018969A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLS REFERENCE:
FURNET APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Frior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1249
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Matches:
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Mismatches:
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    CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SEQ TWARE: PatentIn version 3.2
SEQ ID NO 15
LENGTH: 1448
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: LOCATION: (1393) .. (1393)

: OTHER INFORMATION: n is a, c,

US-10-756-149-15
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ORGANISM: Homo Sapiens
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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US-10-471-010-1
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DB:
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TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REPERENCE: file
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/10650112
| Publication No. US20040110712A1 |
| GENERAL INFORMATION: US/10650112 |
| APPLICANT: MARKOWITZ, Sanford D. |
| TITLE OF INVENTION: METHODS FOR TREATING PATIENTS AND IDENTIFYING THERAPEUTICS |
| FILE REPRENCE: CWARL-POL-04 |
| CURRENT APPLICATION NUMBER: US/10/650,112 |
| FRIOR PILING DATE: 2003-08-26 |
| PRIOR PILING DATE: 2002-10-18 |
| PRIOR PILING DATE: 2002-08-26 |
| PRIOR PILING DATE: 2002-08-26 |
| PRIOR PILING DATE: 2002-08-26 |
| PRIOR PILING DATE: 2002-08-27 |
| NUMBER OF SEQ ID NOS: 27 |
| SEQ ID NO 25 |
| LENGTH: 1212 |
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 1209
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Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Zlocnik, Albert
                                                                                                                NAME/KEY: misc_feature; LCCATION: 1161—
OTHER INFORMATION: n = A,T,C or G
US-11-041-788-9
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                                                        TYPE: DNA
ORGANISM: Homo sapiens
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GORGANISM: HUMAN FOXQ1
US-10-650-112-25
                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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US-10-650-112-25/c
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Pred. No.:
                                                                                                  FEATURE:
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DB:
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NESULT 52

US-10-332-47-61

US-10-332-47

US-10-332-47

US-10-332-47

US-10-32-47

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OTHER INFORMATION: Incyte ID No. US20040053258A1 168827CB1
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Mismatches:
Indels:
Gaps:
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Mismatches:
Indels:
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Matches:
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Matches:
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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9.00
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                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo Bapiens
US-10-471-010-1
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Query Match:
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Query Match:
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Pred. No.:
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Pred. No.:
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US-09-989-890-238 (1-212) x US-10-332-447-61 (1-1818)

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APPLICANT: LA KOVALILON,
PAPLICANT: LA KOVALICO,
APPLICANT: LA KOVALICO,
APPLICANT: Exou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Bachazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 92033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NESCUENCE 26078, Application US/10369493

Sequence 26078, Application US/10369493

PUDIJICATION NO. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Glater, Steven C.

APPLICANT: Glater, Steven C.

APPLICANT: Glodman, Barry S.

APPLICANT: Glodman, Barry S.

APPLICANT: Glodman, WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21
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Matches:
Conservative:
Mismatches:
Indels:
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                                    1685 Treccarcererescerrerer 1711
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24 LeuProSerSerLeuAlaLeuLeuSer 32
                                                                                                                     ; Sequence 90203, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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SEQ ID NO 26078
LENGTH: 2071
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9.00
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ORGANISM: Oryza sativa
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Best Local Similarity:
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US-10-437-963-90203
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Pred. No.:
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Pred. No.:
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DB:
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APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
APPLICANT: GREENE, Barrie D.; SANJAWNALA, Madhu S.;
APPLICANT: GREENE, Barrie D.; SANJAWNALA, Machu S.;
APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;
APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine M.;
APPLICANT: WALSH, Roderick T.; RAWKUMAR, Janice;
APPLICANT: WALSH, Roderick T.; RAWKUMAR, Janice;
APPLICANT: LAL, Preeti; ELLIOTT, VICKI S.; NGUYEN, Danniel B.;
APPLICANT: KHAN, Ferrah A.; KEARNEY, Lian; THANGAVELU, Kavitha;
APPLICANT: KHAN, Ferrah A.; KEARNEY, Lian; THANGAVELU, Kavitha;
APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-0149 USN
CURRENT FILIG DATE: 2003-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATĪON: Incyte ID No. US20040053258A1 7472734CB1
                                                                                                                       US-09-989-890-238 (1-212) x US-10-369-493-26078 (1-2071)
    Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
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                                                                                                                                                                   175 ValLeuValAlaProArgSerThrile 183
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PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PREL PROGRAM
SEQ ID NO 62
LENGTH: 2245
                                                                         Gaps:
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                                                                                                                                                                                                                                                                                                       Sequence 62, Application US/10332447
Publication No. US20040053258A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Percent Similarity:
Best Local Similarity:
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US-10-450-763-15603/c
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                                              Query Match:
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OTHER INFORMATION: 100% homologous to Escherichia coli Spermidine/putrescine OTHER INFORMATION: transport protein A, accession number D90748, Smith-Waterman Score US-10-450-763-15603
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; Sequence 4805, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: Las Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Barbazuk, Brad
; APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: WUMBER: 2003-05-14
; UNMER OF SEQ ID NOS: 204966
; SEQ ID NO 4805
; TEMBER OF SEQ ID NOS: 204966
; TEMBER OF SEQ ID NOS: 204966
; TEMBER OF SEQ ID NOS: 204966
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PLICATION NUMBER: 09/540,217
PRIOR PLICATION NUMBER: 09/540,217
PRIOR PLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NOS: 60736
LENGTH: 2256
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Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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US-10-437-963-4805
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Matches:
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9.00
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100.0%
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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US-11-097-143-23948

Sequence 23948, Application US/11097143

Publication No. US20050208558A1

Publication No. US20050208558A1

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: BETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOO0728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-19

PRIOR PELING DATE: 1999-10-19

PRIOR PELING DATE: 1999-11-12

PRIOR PELING DATE: 1999-11-12

PRIOR PELING DATE: 1999-11-12

PRIOR PELING DATE: 1999-11-12

PRIOR PELING DATE: 2000-01-12

PRIOR PELING DATE: 2000-01-12

PRIOR PELING DATE: 2000-01-22

PRIOR PELING DATE: 2000-01-22

PRIOR PELING DATE: 2000-02-24

PRIOR PELING DATE: 2000-02-24

PRIOR PELING DATE: 2000-02-24

PRIOR PELING DATE: 2000-03-23

WINDERS OF THE DATE: 2000-03-23

WINDERS OF THE DATE: 2000-03-23

WINDERS OF THE DATE: 2000-03-23
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                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_85954C.1 US-10-437-963-86961
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Matches:
Conservative:
Mismatches:
Indels:
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23948
LENGTH: 3840
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                     TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-23948
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                             Alignment Scores:
LENGTH: 3795
                                                                         FEATURE:
                                                                                                                                                                                                       Pred. No.:
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US-10-437-963-86961
; Sequence 86961, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharo, Andrey A.
; APPLICANT: Boukharo, Andrey A.
; APPLICANT: Buckero, Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 86961
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PPLICATION NUMBER: US 60/243,096
PRIOR PPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PRILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREESQ for Windows Version 4.0
SEQ ID NO 691773
LENGTH: 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-989-890-238 (1-212) x US-09-925-065A-691773 (1-2520)
US-09-989-890-238 (1-212) x US-10-437-963-4805 (1-2403)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                             Sequence 691773, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
                                                 25 ProSerSerLeuAlaLeuLeuSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

LOCATION: 1550, 1551

COTHER INFORMATION: n = A,T,C or G

US-09-925-065A-691773
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence 960, Application US/10074095
Publication No. US20030077704A1
| GENERAL INFORMATION:
| APPLICANT: ROBEN et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
| TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
| CURRENT FILING DATE: 2002-02-14
| PRIOR APPLICATION NUMBER: 60/179,065
| PRIOR PELLING DATE: 2000-01-31
| PRIOR APPLICATION NUMBER: 60/180,628
| PRIOR APPLICATION NUMBER: 60/214,886
| PRIOR PILING DATE: 2000-06-28
| PRIOR PILING DATE: 2000-06-28
| PRIOR PILING DATE: 2000-06-38
| PRIOR PILING DATE: 2000-07-16
| PRIOR FILING DATE: 2000-07-26
| PRIOR PILING DATE: 2000-07-26
| PRIOR PILING DATE: 2000-07-26
| PRIOR PILING DATE: 2000-07-11
| PRIOR APPLICATION NUMBER: 60/225,747
| PRIOR PILING DATE: 2000-07-11
| PRIOR FILING DATE: 2000-07-11
| PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                 Sequence 561, Application US/09764860
Sequence 561, Application US/09764860
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT PILING DATE: 2001-01-17
PHIOT APPLICATION 682 I:08
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PATENTIN Ver. 2.0
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Matches:
Conservative:
Mismatches:
Indels:
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       Mismatches:
Indels:
Gaps:
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Best Local Similarity: 100.0%
Query Match: 4.2%
DB:
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9.00
100.0%
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CORGANISM: Homo sapiens
US-09-764-860-961
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Best Local Similarity:
Query Match:
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US-09-764-860-961/c
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US-10-074-095-960/c
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LENGTH: 7880
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TITLE OF INVENTION: DREAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PLILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PLILING DATE: 1999-11-12

PRIOR PLILING DATE: 1999-10-28

PRIOR PLILING DATE: 1999-10-28

PRIOR PLILING DATE: 1999-10-28

PRIOR PLILING DATE: 1999-10-13

PRIOR PLILING DATE: 1999-10-13

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-03-24

PRIOR PLILING DATE: 2000-03-24

PRIOR PLILING DATE: 2000-03-24

PRIOR PLILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOCTWARR: FABESEQ FOR WINGOWS VERSION 4.0

SEQ ID NO 23947
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Patent No. US20020094953A1

GENERAL INFORMATION:

APPLICATT: ROSEN et al.

ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC008

CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1198

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 960

LENGTH: 7880
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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                          Sequence 23947, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
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; ORGANISM: DROSOPHILA
US-11-097-143-23947
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Best Local Similarity:
Query Match:
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US-09-764-860-960/c
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Pred. No.:
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Pred. No.:
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60/225,75 08-14 60/226,86 08-22 1 60/216,64 1 60/216,64 1 60/225,26 1 60/225,26 1 60/225,27 1 60/225,27 1 60/225,27 1 60/251,86 1 2 08	R: 60/235 09-27 R: 60/234 R: 60/234 R: 60/224 R: 60/224 R: 60/224 R: 60/224 R: 60/224 R: 60/224 R: 60/24 R: 60/25	1. 60/23, 03 1. 60/25, 86 1. 60/229, 34 1. 60/229, 34 1. 60/229, 34 1. 60/229, 34 1. 60/229, 34 1. 60/229, 51 1. 60/229, 51 1. 60/229, 51 1. 60/239, 51 1. 60/239, 51 1. 60/239, 50 1. 60/239, 50 1. 60/239, 50 1. 60/239, 50 1. 60/239, 60 1. 60/239, 60
APPLICATION FILING DATE:	APPLICATION FILING DATE: APPLICATION FILING DA	APPLICATION PILING DATE APPLICATION PILING DATE APPLICATION FILING DATE

PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,037
PRIOR APPLICATION NUMBER: 60/237,040
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR APPLICATION NUMBER: 60/239,935
PRIOR PRING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-20
PRIOR PLILING DATE: 2000-10-30
PRIOR PLILING DATE: 2000-10-30
PRIOR PLILING DATE: 2000-10-30
PRIOR PLILING DATE: 2000-11-09
PRIOR PLILING DATE: 2000-11-09
PRIOR PLILING DATE: 2000-11-09
PRIOR PLILING DATE: 2000-10-30
PRIOR PLILING DATE: 2000-11-09
PRIOR PLILING DATE: 2000-08-22
PRIOR PLILING DATE: 2000-08-22
PRIOR PLILING DATE: 2000-08-22
PRIOR PLILING DATE: 2000-08-22
PRIOR PLILING DATE: 2000-08-14
PRIOR PLILING DATE: 2000-11-17
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PRIOR APPLICATION NUMBER: 60/226, 868
PRIOR FILING DATE: 2000-07-07
PRIOR PELICATION NUMBER: 60/216, 647
PRIOR PLICATION NUMBER: 60/216, 647
PRIOR PLICATION NUMBER: 60/216, 880
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-08-14
PRIOR PLING DATE: 2000-08-14
PRIOR PLING DATE: 2000-08-14
PRIOR PLING DATE: 2000-09-17
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-14
PRIOR PLING DATE: 2000-09-17
PRIOR PLING DATE: 2000-09-19
PRIOR PLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/229, 345
PRIOR PLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/229, 345
PRIOR PRIDRE DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230, 300
PRIOR PLING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/230, 300
PRIOR APPLICA
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Sequence 961, Application US/10074095

Publication No. US2003007770441

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PCO08C1

CURRENT APPLICATION NUMBER: US/10/074,095

CURRENT FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: 09/764,860

PRIOR PILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 06/179,065

PRIOR APPLICATION NUMBER: 60/109,065

PRIOR APPLICATION NUMBER: 60/109,659

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-09-14

PRIOR PILING DATE: 2000-09-14

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-14

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PRIOR PILING DATE: 2000-09-14

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-14

PRIOR PILING DATE: 2000-08-14
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR APPLICATION NUMBER: 60/231,414

PRIOR FILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20
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Pred. No.:
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DR FILING DATE: 2000-10-02
DR APPLICATION NUMBER: 60/237,040
DR FILING DATE: 2000-10-02
DR APPLICATION NUMBER: 60/240,960
DR FILING DATE: 2000-10-20
DR APPLICATION NUMBER: 60/239,935
DR FILING DATE: 2000-10-13
DR APPLICATION NUMBER: 60/239,937
DR FILING DATE: 2000-10-13
DR APPLICATION NUMBER: 60/241,787
DR FILING DATE: 2000-10-30
DR APPLICATION NUMBER: 60/244,474
DR FILING DATE: 2000-11-08
DR APPLICATION NUMBER: 60/246,474
DR FILING DATE: 2000-11-08
DR APPLICATION NUMBER: 60/246,474
DR FILING DATE: 2000-11-08
DR APPLICATION NUMBER: 60/246,474
DR FILING DATE: 2000-11-08
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RELING DATE: 2000-11-17

REPLICATION NUMBER: 60/249,217

RELING DATE: 2000-11-17

RELING DATE: 2000-11-17

REPLICATION NUMBER: 60/249,215

REPLICATION NUMBER: 60/249,215

REPLICATION NUMBER: 60/249,264

RELING DATE: 2000-11-17

REPLICATION NUMBER: 60/249,297

RELING DATE: 2000-11-17

RELING DATE: 2000-11-17

REPLICATION NUMBER: 60/249,297

RELING DATE: 2000-11-17

REPLICATION NUMBER: 60/232,400

RELING DATE: 2000-09-14
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R APPLICATION NUMBER: 60/225,213

R PILING DATE: 2000-08-14

R APPLICATION NUMBER: 60/227,182

R FILING DATE: 2000-08-22

R APPLICATION NUMBER: 60/225,214
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RR FILING DATE: 2000-08-14

RR FILING DATE: 2000-11-17

RR PILING DATE: 2000-11-17

RR APPLICATION NUMBER: 60/249,213

RR APPLICATION NUMBER: 60/249,213
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R APPLICATION NUMBER: 60/249,207
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,245
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,244
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/249,216
FILING DATE: 2000-11-17
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FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
FILING DATE: 2000-08-22
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/215,135
FILING DATE: 2000-06-30
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FILING DATE: 2000-09-08
FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/231,414
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FILING DATE: 2000-09-27
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FILING DATE: 2000-09-08
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      PRINCH REPRESENTATION OF PRINCH REPRESENTATION
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC00862
CURRENT APPLICATION NUMBER: US/10/212,872
CURRENT APPLICATION NUMBER: US/10/212,872
CURRENT APPLICATION NUMBER: See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 960
LENGTH: 7880
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PRIOR APPLICATION NUMBER: 60/231,244

PRIOR FILING DATE: 2000-09-08

PRIOR PELLING DATE: 2000-09-14

PRIOR PELLING DATE: 2000-09-14

PRIOR PELLING DATE: 2000-09-14

PRIOR PELLING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 60/232,397

PRIOR PELLING DATE: 2000-09-14

PRIOR PELLING DATE: 2000-09-14

PRIOR PELLING DATE: 2000-09-14

PRIOR PELLING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 60/232,401

PRIOR APPLICATION NUMBER: 60/241,808

PRIOR PELLING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-11-20

PRIOR PELLING DATE: 2000-11-20
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; Sequence 960, Application US/10212872
; Publication No. US200330215893A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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         Sequence 961, Application US/10212872

Publication No. US20030215893A1

GENERAL INFORMATION:

APPLICANT: ROBER et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC008C2

CURRENT APPLICATION NUMBER: US/10/212,872

CURRENT FILING DATE: 2002-08-07

Prior application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 1198

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 961

LENGTH: 7880
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Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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Sequence 411, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OWITA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAW, JUN
APPLICANT: SHIRAW, JUN
APPLICANT: SHIRAW, WONE
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, HROSHI
APPLICANT: SHIRA, DONE
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, 1000 TONE
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: PATTORI, WASAHIRA
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 411
TUPS: NUMBER NUMBER: NUMBER: JENOF
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CORGANISM: Homo sapiens
US-10-212-872-961
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; LOCATION: (1)..(10056)
US-10-156-761-411
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Best Local Similarity:
Query Match:
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Query Match:
   US-10-212-872-961/c
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Pred. No.:
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Sequence 20, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KEASE, MALTHEW R.
TITLE OF INVERTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: 00/022,113
PRIOR FILING DATE: 2000-07-28
NUMBER: OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 20
LENGTH: 10432
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20020119463A1 2700132CB1
US-09-919-172-97
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; OTHER INFORMATION: Incyte ID No. US20030108871A1 2700132CB1
US-09-919-039-20
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Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
Second Control of Application US/09919172

Batent No. US20020119463A1

GENERAL INFORMATION:

APPLICANT: Faris, Mary

APPLICANT: Turner, Christopher M.

TITLE OF INVENTION: PROSTATE CANCER MARKERS;
FILE REFERENCE: PA-0036 US

CURRENT APPLICATION NUMBER: US/09/919,172

CURRENT FILING DATE: 2001-07-30

PRIOR PLICATION NUMBER: 60/222,469

PRIOR PLICATION NUMBER: 2000-07-28

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PERL PROGRAM

SEQ ID NO 97

LENGTH: 10432
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Matches:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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Sequence 262, Application US/10133013

Sequence 262, Application US/10133013

Publication No. US20030166903A1

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Bendman, Olga

APPLICANT: Cocks, Benjamin G.

TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE

FILE REFERENCE: PA.0049 US

CURRENT APPLICATION NUMBER: US/10/133,013

CURRENT PILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: 60/287,067

PRIOR FILING DATE: 2001-04-27

NUMBER OF SEQ ID NOS: 271

SOFTWARE: PERL PROGram

SEQ ID NO 262

LENGTH: 10432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030119009A1 2700132CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 2700132CB1
US-10-133-013-262
                                                                                                                Sequence 349, Application US/10084817

Sequence 349, Application US/10084817

Bublication No. US20030119009A1

GENERAL INFORMATION:

APPLICANT: Sue G. Nuchtern

APPLICANT: Sharon B. Plon

APPLICANT: Jacon M. Shohet

TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION

FILE REFERENCE: PA-0046 US

CURRENT APPLICATION NUMBER: US/10/084,817

CURRENT FILING DATE: 2002-02-25

PRIOR APPLICATION NUMBER: 60/270,784

PRIOR FILING DATE: 201-02-23

NUMBER OF SEQ ID NOS: 365

SOFTWARE: APRL PROGram
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Matches:
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Matches:
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29 AlaLeuLeuSerArgProLeuSerPro 37
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                   US-10-084-817-349/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 349
LENGTH: 10432
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Pred. No.:
Score:
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Sequence 5608, Application US/10723860
; Bublication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5608
; LENGTH: 11466
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      Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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; Publication No. US20040253609A1
; Publication No. US20040253609A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TUTION:
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/10/752,986
; CURRENT APPLICATION NUMBER: US/09/919,172
; PRIOR APPLICATION NUMBER: US/09/919,172
; PRIOR PELLING DATE: 2001-07-30
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 2700132CB1
                                                                                                                                                                            5063 GCTCTTCTTTCACGCCCACTTTCCCCA 5037
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                                                                                                                                             29 AlaLeuLeuSerArgProLeuSerPro 37
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CORGANISM: Homo sapiens
US-10-723-860-5608
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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US-10-723-860-5608/c
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LENGTH: 10432
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APPLICANT: Vesustus Forschungs Cie. Translational Cancer Research GmbH
TITLE OF INVENTION: Antisense oligonuclectides for treating proliferating cells
FILE REFERENCE: PA32470US-01938
CURRENT APPLICATION NUMBER: US/10/739,946
CURRENT FILING DATE: 1998-05-22
RICH REILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 1
LENGTH: 12493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030190640A1 412661.2
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US-10-252-157-263/c

Sequence 263, Application US/10252157

Sequence 263, Application US/10252157

GENERAL INFORMATION

APPLICANT: Faris, Mary

APPLICANT: Pearson, Cecelia I.

TILLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER;

FILE REFERENCE: PA-002-10-10S

CURRENT APPLICATION NUMBER: US/10/252,157

CURRENT FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

PRIOR FILING DATE: 2002-10-01

NUMBER OF SEQ ID NOS: 501

SOFTWARE: PERL Program
                 US-09-989-890-238 (1-212) x US-10-719-993-403 (1-11602)
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Mismatches:
Indels:
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Matches:
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; Publication No. US20040242519A1
; GENERAL INFORMATION:
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; LOCATION: (197)...(9964)
US-10-739-946-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 12494
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Pred. No.:
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Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER:
US/10/719,993
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 402
LENGTH 11598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 403, Application US/10719993

Publication No. US20040265849A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: C1001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT FILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 403

ENGTH: 11602
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               Length:
Matches:
Conservative:
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ORGANISM: Homo sapiens
                                                 Percent Similarity:
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Best Local Similarity:
Query Match:
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Alignment Scores:
Pred. No.:
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Length:
Matches:
Conservative:
Mismatches:

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Gaps:

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; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20030113720A1 g415818
US-09-918-624B-48
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Best Local Similarity:
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US-09-918-624B-48/C
| Sequence 48, Application US/09918624B
| Sequence 48, Application US/09918624B
| Publication No. US20030113720A1
| GENERAL INFORMATION:
| APPLICANT: Schebye, Xiao Min
| APPLICANT: Schebye, Xiao Min
| APPLICANT: Schebye, Thierry
| TITLE OF INVENTION: CUBAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
| FILE REFERENCE: PA-0033 US
| CURRENT FILING NUMBER: US/09/918,624B
| CURRENT FILING DATE: 2002-12-03
| PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                Sequence 18, Application US/10115831
| Sequence 18, Application US/10115831
| Publication No. US20030219743A1
| GENERAL INFORMATION:
| APPLICANT: Tang, Y. Tom
| APPLICANT: Asundi, Vinod
| APPLICANT: Ren, Feiyan
| APPLICANTION: No. US20030219743A1e1 Nucleic Acids and
| TILLE OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
| TILLE OF INVENTION: POLYPEPTION
| CURRENT APPLICATION NUMBER: US/10/115, 831
| CURRENT FILING DATE: 2000-04-02
| PRIOR APPLICATION NUMBER: 09/667, 298
| PRIOR APPLICATION NUMBER: 09/667, 298
| PRIOR APPLICATION NUMBER: 09/577, 408
| PRIOR APPLICATION NUMBER: 09/577, 408
| NUMBER OF SEQ ID NOS: 178
| UNMBER OF SEQ ID NOS: 178
| LENGTHARE: PLE_genes Version 2.0
| SEQ ID NO 18
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       Mismatches:
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SOFTWARE: PERL Program
SEQ ID NO 48
LENGTH: 12515
TYPE: DNA
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; LOCATION: (197)..(9967)
US-10-115-831-18
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ORGANISM: Homo BapienB
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Best Local Similarity:
Query Match:
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RESULT 81
US-09-566-007A-989/C

i Sequence 9894, Application US/09968007A

i Publication No. US20040115625A1

i GENERAL INFORMATION:

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signs

TITLE OF INVENTION: Gene Sets

FRICK APPLICATION NUMBER: US/60/237,172

FRIOR PELING DATE: 2000-10-02

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-02

FRIOR FILING DATE: 2000-10-02

FRIOR FILING DATE: 2000-10-02

FRIOR FILING DATE: 2000-10-02

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE
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US-09-989-890-238 (1-212) x US-09-918-624B-48 (1-12515)
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; Sequence 313, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INPORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Offire B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.32e+03
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US-09-968-007A-989
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Pred. No.:
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; LOCATION: (1). (12515)
; OTHER INFORMATION: n=a,t,g or
US-10-843-641A-7459
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 58
LENGTH: 12515
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APPLICANT: BIRNBAUM, DANIEL
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL00149E; US/10/719,993
CURRENT APPLICATION NUMBER: US/10/719,993
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Sequence 7459, Application US/10843641A
Sequence 7459, Application US/10843641A
Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using TITLE OF INVENTION: Signature Gene Sets
APPLICANT: Shak, Steve
APPLICANT: Walker, Michael Graham
TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
FILE REFERENCE: 39740-0001US
CURRENT PILING DATE: 2003-012
PRIOR PILING DATE: 2003-09-18
PRIOR PILING DATE: 2002-09-18
PRIOR PILING DATE: 2002-09-18
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 384
NUMBER OF SEQ ID NOS: 384
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 405
LENGTH: 12515
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CORGANISM: Homo sapiens
US-10-719-993-405
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Query Match:
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Best Local Similarity:
Query Match:
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LENGTH: 12515
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Pred. No.:
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Pred. No.:
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US-10-843-
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APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: JACQUEMIER, JOCELYNE
APPLICANT: GINESTIER, CHRISTOPHE
APPLICANT: GINESTIER, CHRISTOPHE
APPLICANT: DEBONO, SIECHALIE
TITLE OF INVENTION: IDENTIFICATION OF AN ERBEZ GENE EXPRESSION SIGNATURE IN
TITLE OF INVENTION: BREAST CANCERS
FILE REFERENCE: 1308-P-03
CURRENT APPLICATION NUMBER: US/10/928,465
CURRENT APPLICATION NUMBER: US 60/498,497
PRIOR PILING DATE: 2003-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 8447
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Mismatches:
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FILE REFERENCE: 689290-189

CURRENT APPLICATION NUMBER: US/10/843,641A

CURRENT FILING DATE: 2004-05-12

PRIOR FILING DATE: 2001-06-05

PRIOR PLILOGATION NUMBER: US/09/954,531

PRIOR PLILNG DATE: 2001-09-18

PRIOR PLILNG DATE: 2001-09-18

PRIOR PELICATION NUMBER: US/09/954,456

PRIOR PELING DATE: 2001-09-25

PRIOR PLING DATE: 2001-09-25

PRIOR PLILNG DATE: 2001-09-26

PRIOR PLILNG DATE: 2001-09-26

PRIOR PLILNG DATE: 2001-09-26

PRIOR PLILNG DATE: 2001-09-26

PRIOR PLILNG DATE: 2001-09-27

PRIOR PLILNG DATE: 2001-09-28

PRIOR PLILNG DATE: 2001-09-28

PRIOR PLILNG DATE: 2001-09-28

PRIOR PLILNG DATE: 2001-00-02

PRIOR PLILNG DATE: 2001-10-02

PRIOR PLILNG DATE: 2001-10-03

PRIOR PLILNG DATE: 2001-10-03
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Publication No. US20050089899A1
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Sequence 6886, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: ALTHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALTHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT APPLICATION NUMBER: US/10/719,993
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FREESE FESTSEQ FOR Windows Version 4.0
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Publication No. US20030224516A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION ANTISENSE MODULATION OF PROX-1 EXPRESSION
FILE REFERENCE: RTS-0421
CURRENT APPLICATION NUMBER: US/10/162,846
CURRENT FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 134
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                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-404
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US-10-719-993-6886
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-719-993-6886/c
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   LENGTH: 12678
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Pred. No.:
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Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL ALGARILY
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01496
CURRENT APPLICATION NUMBER: US/10/719,993
NUMBER OF SEQ ID NOS: 55342
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FastSEQ for Windows Version 4.0
                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA sequence
                                               FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (12515)
OTHER INFORMATION: antigen identified by monoclonal antibody
OTHER INFORMATION: ki-67 (MKI67) gene.
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OTHER INFORMATION: Incyte ID No. US20020192678A1 412661.2
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Conservative:
Mismatches:
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Matches:
Conservative:
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TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE
FILE REPERENCE: PA-0043 US
CURRENT APPLICATION NUMBER: US/10/071,766
CURRENT PILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 144
SEQ ID NO 49
LENGTH: 12632
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Publication No. US20020192678A1
GENERAL INFORMATION:
ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Best Local Similarity:
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NAME/KEY: misc feature
LOCATION: (20780)..(20799)
OTHER INFORMATION: "n" at positions 20780 through 20799 can be any base.
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US-09-997-722-85
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      INFORMATION: "n" at positions 7789 through 7808 can be any
                                                                                be any
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NAME/KEY: misc_feature
LOCATION: (33786)..(33805)
OTHER INFORMATION: "n" at positions 33786 through 33805 can be
                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (27797)..(27816)
OTHER INFORMATION: "n" at positions 27797 through 27816 can be
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (31149)..(31168)
OTHER INFORMATION: "n" at positions 31149 through 31168 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRATURE:
NAME/KEY: misc_feature
LOCATION: (34873)..(34892)
OTHER INFORMATION: "n" at positions 34873 through 34892 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (50121)..(50140)
OTHER INFORMATION: "n" at positions 50121 through 50140 can be
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                                                                                                                                                           positions 14125 through 14144 can be
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LOCATION: (53877)..(53896)
OTHER INFORMATION: "n" at positions 53877 through 53896 can
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LOCATION: (45961)..(45980)
OTHER INFORMATION: "n" at positions 45961 through 45980 can
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LOCATION: (57012)..(57031)
OTHER INFORMATION: "n" at positions 57012 through 57031 can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            positions 60915 through 60934 can
                                                                              positions 9978 through 9997 can
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Matches:
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Mismatches:
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LOCATION: (14125)..(14144)
OTHER INFORMATION: "n" at ]
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LOCATION: (60915)..(60934)
OTHER INFORMATION: "n" at )
                                        NAME/KEY: misc feature
LOCATION: (9978)..(9997)
OTHER INFORMATION: "n" at
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LOCATION: (55271)..(55290)
OTHER INFORMATION: "n" at
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                                                                                                                                                                                                                                                                                                              APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLBIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01044-US
FULE REFERENCE: CLO01044-US
CURRENT APPLICATION NUMBER: US/10/471,010
CURRENT APPLICATION NUMBER: US/09-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 85, Application US/0999722;
Publication No. US20040072154A1;
Fublication No. US20040072154A1;
GENERAL INFORMATION:
APPLICANT: MOTIB, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REPERENCE: A.71171/RMS/DCF;
CURRENT APPLICATION NUMBER: US 09/797722
CURRENT FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR PLIING DATE: 2001-11-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 96600
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      Conservative:
Mismatches:
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Gaps:
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Mismatches:
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Matches:
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                                                                                                                                       24 LeuProSerSerLeuAlaLeuLeuSer 32
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OTHER INFORMATION: n = A,T,C or
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ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (7789)..(7808)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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Percent Similarity:
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LENGTH: 73544
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US-10-471-010-3
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Publication No. US20050181389A1

GENERAL INFORMATION:

APPLICANT: Harris, Cole

APPLICANT: Davis, Lisa

TITLE OF INVENTION: Compositions and Methods for Glioma Classification

FILE REFERENCE: 03-968-US

CURRENT APPLICATION NUMBER: US/10/981,277

CURRENT PELIANG DATE: 2004-11-03

PRIOR FILING DATE: 2003-11-03

NUMBER OF SEQ ID NOS: 57

SOFTWARE: PatentIn version 3.3

SEQ ID NO 31

LENGTH: 183046
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Matches:
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Matches:
Conservative:
Mismatches:
Indels:
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JOS-10-156 / 10-156/3/C

JOS-10-156 / 10-156/2
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-15103
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; ORGANISM: Homo sapiens
US-10-981-277-31
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Best Local Similarity:
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Best Local Similarity:
RESULT 92
US-10-156-761-15103/c
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DB:
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) LOCATION: (1)...(493999)
, OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-719-993-6787
                                                                                                                                                            105-10-719-993-6787/c

| Sequence 6787, Application US/10719993
| Publication No. US20040265849A1
| Publication No. US20040265849A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al. | TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH | TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF | FILE REPERENCE: CL001496 | CURRENT APPLICATION NUMBER: US/10/719,993 | CURRENT PILING DATE: 2003-11-24 | NUMBER OF SEQ ID NOS: 55342 | SOFTWARE: FastSEQ for Windows Version 4.0 | SOFTWARE: FastSEQ for Windows Version 4.0 | SOFTWARE: PASTSEQ for Windows Versio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-989-890-238 (1-212) x US-10-719-993-6787 (1-493999)
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167188 AGAGCCCTTCCATCCTTAGCCCTC 167162
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Matches:
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APPLICANT: IKEDA, HARUO
APPLICANT: BHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERRNCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
SRO ID NO 1 SECOLO NOS: 15109
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Publication No. US20030119018A1
GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (4187715)
CTHER INFORMATION: a, t, c,
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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RESULT 99
US-11-036-317-687056
i Sequence 687056, Application US/11036317
i Publication No. US20050214823A1
i GENERAL INFORMATION:
    APPLICANT: Williams, Alan
    APPLICANT: Williams, Alan
    TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
    FILE REFERENCE: 3624.1
    CURRENT APLICATION NUMBER: US/11/036,317
    FRIOR APPLICATION NUMBER: US 60/536,639
    PRIOR PILING DATE: 2004-01-13
    NUMBER OF SEQ ID NOS: 991174
    SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
    SEQ ID NO 687056
                                                                                                                                                                                                                                         APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REPERENCE: 3654.11
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR PPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SEQ ID NO 69571
LENGTH: 25
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; ORGANISM: Mus musculus
US-11-036-317-669571
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; ORGANISM: Mus musculus
US-11-036-317-687056
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Sequence 669570, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:

APPLICANT: Williama, Alan

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT PILING DATE: 2005-01-13

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

LENGTH: 25
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Sequence 172651, Application US/10719900

Publication No. US20050026164A1

GENERAL INFORMATION:
TILLE OF INVERTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 35281.

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT PILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

FROM REING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SEQ ID NO 172651

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; ORGANISM: Mus musculus
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; ORGANISM: Mus musculus
US-11-036-317-669570
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RESULT 100
US-10-131-827-69
i Sequence 69, Application US/10131827
i Publication No. US2004009479A1
j GENERAL INFORMATION:
i APPLICANT: Woldgemuth, Jay
i APPLICANT: Woldgemuth, Jay
i APPLICANT: Wordward, Robert
i APPLICANT: Wordward, Robert
i TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
i TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
i TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
i TITLE OF INVENTION NUMBER: US 10/006,290
i CURRENT APPLICATION NUMBER: US 10/006,290
i PRIOR PRIING DATE: 2001-06-08
i PRIOR FILING DATE: 2001-06-08
i NUMBER OF SEQ ID NOS: 9090
i SEQ ID NO 69
i SEQ ID NO 69
i MANDEL PATENTIN VERSION 3.1
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29 AlaLeuLeuSerArgProLeuSer 36
                         1 GCGCTGCTGAGTAGCCTCTCTCT 24
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GRGANISM: Homo sapiens
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Sequence 25234, A
Sequence 353884,
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Sequence 608, App
Sequence 84711,
Sequence 97, App1,
Sequence 223, App
Sequence 15, App1
Sequence 15, App1
Sequence 61675,
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                                                                            Sequence 3594, Ap Sequence 22366, A Sequence 468689, Sequence 48878, A Sequence 48878, A Sequence 9, Appl 1 Sequence 53796, A Sequence 53796, A Sequence 53796, A
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Sequence 173, A
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Sequence 172, A
Sequence 135, A
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2 US-11-124-367A-3389
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2 US-11-124-367A-3389
2 US-11-124-367A-23366
2 US-11-124-367A-23366
2 US-10-925-065A-428878
2 US-10-925-065A-428878
2 US-10-925-065A-48878
2 US-10-925-065A-48878
2 US-10-925-065A-61173
2 US-10-750-185-48878
2 US-11-124-368A-137
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US-09-925-065A-630748
US-09-925-065A-893900
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-Q=/abse/ABSSWEB_gool/US09989890/runat_leatap -SUFFIX=oligo_p2n.rmpbn
-MINMATCH=0.1_-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=500 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abse05h
-USER=US09999890 @CGN 1 1411 @runat 16032006_095523_17709 -NCPU=6 -ICPU=3
-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-NO MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=17
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Sequence 2250, Ap
Sequence 2364, Ap
Sequence 2475, Ap
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Matches:
Conservative:
Mismatches:
Indels:
                                              APPLICANT: OTSURA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: TAMECHIKA, KAORU
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, TSUTOMU
APPLICANT: SEKI, NAOHIKO
APPLICANT: SOSHIKAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NASHO, YASUHIKO
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR PILING DATE: 2005-03-07
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PALENT OF SEQ ID NOS: 4096
SOFTWARE: PALENT OF SEQ ID NOS: 4096
SERNOTH: 1785
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; ORGANISM: Homo Bapiens
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US-11-124-367A-3389/C
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US-11-124-367A-3389/C
US-11-124-367A-3389/C
Sequence 3389, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses THIR DETERMINED THING DATE: 2004-05-09
CURRENT TILING DATE: 2004-05-07
PRIOR PLILNG DATE: 2004-05-07
PRIOR PLILNG DATE: 2004-06-25
PRIOR PLILNG DATE: 2004-06-25
PRIOR PLILNG DATE: 2004-06-25
PRIOR PLILNG DATE: 204-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: Fastsed for Windows Version 4.0
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Publication No. US20060024700A1

GENERAL INFORMATION:
APPLICANT: Michele Cargili
APPLICANT: Honglin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01519-ORD
CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT PILING DATE: 2005-05-09

FRIOR APPLICATION NUMBER: US 60/568,846

FRIOR FILING DATE: 2004-05-07
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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               TYPE: DNA
CORGANISM: Homo sapiens
US-11-124-368A-17847
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Pred. No.:
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LENGTH: 201
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Sequence 2475, Application US/11124368A

Sequence 2475, Application US/11124368A

Publication No. US20050287559A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill

APPLICANT: James J. Devlin

APPLICANT: May Luke

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

CURRENT FILING DATE: 2005-05-09

PRIOR PLILOR DATE: 2004-05-07

PRIOR PLILOR DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SOUTHARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 2475

LENGTH: 201
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US-11-124 368A-17847

Squence 17847, Application US/11124368A

Squence 17847, Application US/11124368A

Publication No. US20050287559A1

GENERAL INFORMATION:
APPLICANT: Michele Cargill

APPLICANT: May Luke

TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CLOO1524

CURRENT APPLICATION NUMBER: US/11/124,368A

CURRENT FILING DATE: 2005-05-09

PRIOR PILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-11-09
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
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Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17847
                                                                                                                                                                                     29 AlaLeuLeuSerArgProLeuSerPro 37
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ORGANISM: Homo sapiens
                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Alignment Scores:
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CLOO1219,ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
FRIOR PELLOR DATE: 2004-05-09
FRIOR PELLOR DATE: 2004-05-07
FRIOR PILING DATE: 2004-06-05
FRIOR APPLICATION NUMBER: US 60/582,609
FRIOR APPLICATION NUMBER: US 60/599,554
FRIOR PILING DATE: 2004-06-09
FRIOR PILING DATE: 2014-06-09
FRIOR PILING DATE: 2014-06-
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT PRILING DATE: 2001-08-08
FRIOR PAPLICATION NUMBER: US 60/243,096
PRIOR PAPLICATION NUMBER: US 60/243,096
PRIOR PALING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2000-11-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PELING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 468689
LENGTH: 637
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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; Sequence 468689, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-124-367A-22366
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Best Local Similarity:
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Sequence 3594, Application US/11124367A

Publication No. US20060024700A1

GENERAL INFORMATION:
APPLICANT: Michele Cargill

APPLICANT: Hongjin Huang

TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01519, ORD

CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT FILING DATE: 2005-05-09

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07

PRIOR PLING DATE: 2004-06-05

PRIOR PLING DATE: 2004-06-05

NUMBER OF SEQ ID NOS: 34460

SOFTWARE: PRESEQ FOR Windows Version 4.0

SEQ ID NO 3594
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Matches:
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Mismatches:
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-69
PRIOR PILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 3491
LENGTH: 201
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APPLICANT: Hongjin Huang
                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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Pred. No.:
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DB:
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Alignment Scores:
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LENGTH: 1209
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DB:
   Pred. No.:
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                                                                                                                                               Sequence 726141, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108047.135

CURRENT PELING DATE: 2001-08-08

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-01

SRIOR FILING DATE: 2001-01-01

SRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SEQ ID NO 726141

LENGTH: 652
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US-10-750-185-48878

Sequence 48878, Application US/10750185

Publication No. US20050260603A1

GENERAL INPORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DenisE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TILE REFERENCE: MMILLOO-2
CURRENT FILING DATE: 2003-12-31
FRIOR APPLICATION NUMBER: US 60/437,482
FRIOR PELING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 48878
FUNDA ABBRITANTA
SEQ ID NO 48878
FUNDA ABBRITANTA
SERVENCE: NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 48878
FUNDA ABBRITANTA
SEQ ID NO 48878
FUNDA ABBRITANTA
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
497 CCGAGCTCCCTGGCTCTATCCAGG 471
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US-10-750-185-48878
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Best Local Similarity:
Query Match:
DB:
                                                                                                    RESULT 11
US-09-925-065A-726141/c
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US-10-750-623-48878
US-10-750-623-48878
Sequence 48878, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MI GENONICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: RESR, Richard
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
TILE TRYBENCE: MM11100-1
CURRENT PILING DATE: 2003-12-31
CURRENT PILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 48878

LENGTH. 718
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Sequence 9, Application US/10649591

Sequence 9, Application US/10649591

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: CATEGORIZING PATIENTS

TITLE OF INVENTION: CATEGORIZING PATIENTS

TITLE OF INVENTION: CATEGORIZING PATIENTS

CURRENT APPLICATION NUMBER: US/10/649,591

CURRENT FILING DATE: 2002-08-26

PRIOR FILING DATE: 2002-08-26

PRIOR FILING DATE: 2002-08-26

PRIOR FILING DATE: 2002-10-18

NUMBER OF SEQ ID NOS: 22

SOFTWARE: FRSESEQ FOR WINGONS Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
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                                                                                                     Gaps:
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Percent Similarity:
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Query Match:
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Best Local Similarity:
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT PILING DATE: 2003-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER: OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 53796
LENGTH: 2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-989-890-238 (1-212) x US-10-750-185-53796 (1-2888)
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                                           DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
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Best Local Similarity:
Query Match:
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Pred. No.:
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Publication No. US20040181048A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR PRIOR FILING DATE: 2001-01-6

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Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 53796, Application US/10750185
; Publication No. US20050260603A1
                                                                                                                          ; OTHER INFORMATION: n = A, T, C or G
US-10-649-591-9
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LOCATION: 1550, 1551
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                             FEATURE:
NAME/KEY: misc_feature
LOCATION: 1161
                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
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US-09-925-065A-691773
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Length:
Matches:
Conservative:
Mismatches:
Indels:

100.0%

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Sequence 53796, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: MERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: ROSENFELD, David
; APPLICANT: RATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; TILLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REPERENCE: MAILIOG-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT PILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; ROWERS OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 53796
; LINCTH: 2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-989-890-238 (1-212) x US-10-750-623-53796 (1-2888)
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Bovine 19866880672526
US-10-750-623-53796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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squence 136, Application US/11124368A

publication No. US20050287559A1

GENERAL INPORMATION:

APPLICANT: May hitchele Cargill

APPLICANT: James J. Devlin

APPLICANT: May Luke

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

FILE REFERENCE: CLO01524

CURRENT FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR PLILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

NUMBER OF SEQ ID NOS: 21112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 136

LEMOTH: 11602
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Sequence 172, Application US/11124367A

Publication No. US20060024700A1

GENERAL INFORMATION:
APPLICANT: Michele Cargill

APPLICANT: Michele Cargill

APPLICANT: Monglin Huang

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Pibrosis Methods of Detection and Uses Thereof

FILE REPERENCE: CLOO1519.0RD

CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT APPLICATION NUMBER: US 60/568,846

FRIOR APPLICATION NUMBER: US 60/589,846

FRIOR FILING DATE: 2004-05-07

FRIOR FILING DATE: 2004-06-07

FRIOR PILING DATE: 2004-06-07

FRIOR PILING DATE: 2004-06-08

NUMBER OF SEQ ID NOS: 34460

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 34460

SEQ ID NOS: 34460
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                                                          US-09-989-890-238 (1-212) x US-11-124-367A-173 (1-11598)
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Mismatches:
Indels:
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; ORGANISM: Homo sapiens
US-11-124-368A-136
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CORGANISM: Homo Sapiens
US-11-124-367A-172
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Query Match:
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US-11-124-367A-172/c
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                                                                                       Sequence 137, Application US/11124368A;
Sequence 137, Application WS/20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: May Luke
TITLE OF INVENTION: Generic Polymorphisms Associated with
TITLE OF INVENTION: Generic Polymorphisms Associated with
TITLE OF INVENTION: Wascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CL001524
CURRENT PILING DATE: 2005-05-09
PRIOR PILING DATE: 2004-05-07
PRIOR PLILOR DATE: 2004-11-09
NUMBER: US 60/568,845
PRIOR PLILOR DATE: 2004-11-09
NUMBER: PSEC ID NOS: 21112
SOFTWARE: FSEC ID NOS: 21112
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Sequence 173, Application US/11124367A

Publication No. US20066024700A1

GENERAL INFORMATION:

APPLICANT: Michaele Cargill

FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof

FILE REFERENCE: CL00159.0RD

CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT APPLICATION NUMBER: US/6/568,846

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-25

PRIOR FILING DATE: 2004-06-09

NUMBER OF SEQ ID NOS: 34460

SOFTWARE: FascEGQ for Windows Version 4.0

SERVICE: FILE CARGING 
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Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
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846 TCTTCCTTAGCACTTCTATCACGACCA 872
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; ORGANISM: Homo Sapiens
US-11-124-367A-173
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APPLICANT: Michaele Cargill

APPLICANT: James J. Devlin

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

FILE REFERENCE: CLOO1524

CURRENT APPLICATION NUMBER: US/11/124,368A

CURRENT PILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR APPLICATION NUMBER: US 60/625,936

PRIOR PILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07
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US-11-124-367A-5068/c
US-11-124-367A-5068/c
is dequence 5066, Application US/11124367A
is bublication No. US20060024700A1
is deblication No. US20061024700A1
is APPLICANT: Michele Cargill
is APPLICANT: Honglin Huan
is APPLICANT: Honglin Huan
is TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
is TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
is TITLE OF INVENTION: Fibrosis Wethods of Detection and Uses Thereof
is TITLE OF INVENTION: Fibrosis Wethods of Detection and Uses Thereof
is CURRENT FILING DATE: 2005-05-09
is PRIOR PILING DATE: 2004-05-07
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SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 171
; LENGTH: 12678
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-124-367A-171
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LENGTH: 41041
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Pred. No.:
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sequence 135, Application US/11124368A

publication No. US20050287559A1

GENERAL INFORMATION:

APPLICANT: Michele Cargill

APPLICANT: May Luke

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof

CURRENT PELICATION NUMBER: US 60/568,845

PRIOR PILING DATE: 2004-05-07

PRIOR PILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 135

LEAGTH: 12678
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ORGANISM: Homo sapiens
                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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Query Match:
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US-11-124-368A-135/c
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      Alignment Scores:
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Publication No. US20050287570A1

Publication No. US20050287570A1

APPLICANT: Myeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (AMJ01086)

CURRENT APPLICATION NUMBER: US/11/136,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 261, Application US/10330773
; Sequence 261, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
    APPLICANT: David W. Morris
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; FILE REFERENCE: 529452010300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SEQ ID NO 261
; SEQ ID NO 261
; LENGTH: 215248
                                                                                                                                                                                                                                                                                                                                                                                   US-09-989-890-238 (1-212) x US-11-124-367A-5068 (1-41041)
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-99
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5668
LENGTH: 41041
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LOCATION: (1)...(215248)
OTHER INFORMATION: n = A,T,C or G
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100.0%
4.2%
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9.00
100.0%
100.0%
                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5068
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Best Local Similarity:
Query Match:
DB:
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Query Match:
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US-10-330-773-261
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US-11-103-122-44/c

Sequence 44, Application US/11103122

Sequence 44, Application US/11103122

Sequence 44, Application US VISIO050282190A1

Sequence 44, Application US VISIONA

GENERAL INFORMATION:

APPLICANT: Els, John T.

APPLICANT: Lis, John T.

TITLE OF INVENTION: MODIGAR DESIGN AND CONSTRUCTION OF NUCLEIC ACID CONSTRUCTS, TITLE OF INVENTION: MOLECULES, APTAMER-DERIVED NUCLEIC ACID CONSTRUCTS, TITLE OF INVENTION: SCAFFOLDS, THEIR EXPRESSION, AND METHODS OF USE FILE REFERENCE: 19603/4491

CURRENT APPLICATION NUMBER: US/11/103,122

CURRENT FILING DATE: 2006-04-11

PRIOR FILING DATE: 2006-04-11

PRIOR FILING DATE: 2004-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Aptabody-B4/S1/101
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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CURRENT FILING DATE: 2005-05-25
PRIOR PEDILCATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SSCTWARE: Patentin version 3.2
SEQ ID NO 359961
LENGTH: 25
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
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8.00
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                                                                                                                                             TYPE: DNA ORGANISM: Artificial
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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LENGTH: 198
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Sequence 2791, Application US/11124367A

Publication No. US20060024700A1

GENERAL INFORMATION:
APPLICANT: Michela Cargill
APPLICANTON: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: C1001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT APLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR PILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: PSSEC for Windows Version 4.0
SEQ ID NO 24791

LENGTH: 201
## APPLICANT: Hongjin Huang
## TITLE OF INVENTION: Genetic Polymorphisms Associated with
## TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
## FILE REFERENCE: CL001519 CND
## CURRENT APPLICATION NUMBER: US/11/124,367A
## CURRENT APPLICATION NUMBER: US/11/124,367A
## CURRENT APPLICATION NUMBER: US/0568,846
## PRIOR APPLICATION NUMBER: US 60/582,609
## PRIOR APPLICATION NUMBER: US 60/582,609
## PRIOR APPLICATION NUMBER: US 60/599,554
## PRIOR APPLICATION NUMBER: US 60/599,554
## PRIOR PILING DATE: 2004-06-09
## NUMBER OF SEQ ID NOS: 34460
## SEQ ID NO 24790
## SEQ ID NO 24790
## ILENGTH: 201
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Matches:
Conservative:
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Indels:
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; ORGANISM: Homo sapiens
US-11-124-367A-24790
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Best Local Similarity:
Query Match:
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Query Match:
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Pred. No.:
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123 AGACCACTCTCCCTCCACCTGCC 146

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WS-11-124-367A-25234

Sequence 25234, Application US/11124367A

Publication No. US20060024700A1

Sequence 25234, Application US/11124367A

Publication No. US20060024700A1

APPLICANT: Michele Cargill

APPLICANT: Michele Cargill

APPLICANT: Michele Cargill

TITLE OF INVENTION: Genetic Polymorphisms Associated with

TITLE OF INVENTION: Elbrosis Methods of Detection and Uses Thereof

TITLE OF INVENTION: Elbrosis Methods of Detection and Uses THER ENERGY COURENT PLING DATE: 2005-05-09

CURRENT FILING DATE: 2005-05-09

PRIOR PELICATION NUMBER: US 60/568,846

PRIOR APPLICATION NUMBER: US 60/582,609

PRIOR APPLICATION NUMBER: US 60/582,609

PRIOR APPLICATION NUMBER: US 60/599,554

PRIOR PILING DATE: 2004-06-25

PRIOR PILING DATE: 2004-08-09

SOFTWARE PARES FASES for Windows Version 4.0

SEQ ID NO 22234
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nacleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827,135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-24
FRIOR PILING DATE: 2000-11-20
FRIOR PILING DATE: 2000-11-20
FRIOR PILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-6
FRIOR FILING DATE: 2001-11-6
FRIOR FILING DATE: 2001-11-6
FRIOR FILING DATE: 2001-01-16
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Matches:
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1 LOCATION: 200

1 CTHER INFORMATION: n = A,T,C or G

US-09-925-065A-620441
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; ORGANISM: Homo sapiens
US-11-124-367A-25234
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Best Local Similarity:
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US-09-925-065A-363885
Sequence 363885, Application US/09925065A
Sequence 363885, Application US/09925065A
Sequence 363886, Application No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
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Matches:
Conservative:
Mismatches:
Indels:
         Length:
Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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US-09-925-065A-363884
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Alignment Scores:
Pred. No.:
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Pred. No.:
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US-09-925-065A-363886

Sequence 363886, Application US/09925065A

PUBLICALION NO. USZO04018104BA1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Udentification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphlsms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphlsms in the Human Genome

TITLE OF INVENTION: US 00/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/280,846

PRIOR APPLICATION NUMBER: US 60/280,846
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREESEQ for Windows Version 4.0
SSOFTWARE: 377
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; ORGANISM: Homo sapiens
US-09-925-065A-363885
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CORGANISM: Homo sapiens
US-09-925-065A-363886
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Best Local Similarity:
Query Match:
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Query Match:
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US-11-043-752-949/c
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Pred. No.:
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Sequence 844771, Application US/09925065A; Sequence 844771, Application US/09925065A; Publication No. US20040181048A1
GENERAL INPOWATION:
I SERVELL INPOWATION:
I TITLE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REPERRNCE: 10827.135
CURRENT FILING DATE: 2001-08-08
PRIOR PLLING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PLLING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR SEQ IN NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-01-05-09
NUMBER OF SEQ IN NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 97, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Penger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT APPLICATION NUMBER: US/10/623,155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
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       Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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   Percent Similarity:
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Query Match:
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Best Local Similarity:
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LENGTH: 408
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Pred. No.:
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LENGTH: 441
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US-11-000-688-608
Sequence 608, Application US/11000688
Publication No. US20050287544A1
Sequence 608, Application Wo. US20050287544A1
SEGUENCE INFORMATION:
APPLICANT: BERTUCCI, Francois
APPLICANT: HOULGATTE, Remi
APPLICANT: BINNBAUM, Daniel
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
FILLE REFERENCE: 1423-R-03
CURRENT APPLICATION NUMBER: US/11/000,688
CURRENT PILING DATE: 2004-12-01
PRIOR PILING DATE: 2003-12-01
NUMBER OF SEQ ID NOS: 1596
SOFTWARE: Patentin version 3.2
SEQ ID NO 608
LENGTH: 406
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NAME/KEY: misc_feature
LOCATION: [1)...(406)
CTHER INFORMATION: 5, terminal sequence from clone
OTHER INFORMATION: image:283375. calcium channel, voltage-dependent,
OTHER INFORMATION: alpha 11 subunit(CACNAII) gene.
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ORGANISM: Artificial Sequence
FEATURE:
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US-11-043-752-949
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
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US-09-925-065A-489934/c
is Sequence 489934, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
APPLICANT: Wars, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
; TITLE OF INVENTION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: PRESEE for Windows Version 4.0
; SEQ ID NO 489934
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Matches:
Conservative:
Mismatches:
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Matches:
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Sequence 223, Application US/10667295
Sequence 221, Application US/20650257293A1
GENERAL INFORMATION:
APPLICANT: Mascia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REPERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
                                                                                                                                                                                                                                                                               US-09-989-890-238 (1-212) x US-10-623-155-97 (1-441)
                                                                                                                                                                                                                                                                                                                   268 AGCTCTTTGGCTCTGCTCAGCAGG 245
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             FEATURE:

NAME/KEY: misc feature

LOCATION: 12, 308

OTHER INFORMATION: n = A,T,C or G
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US-09-925-065A-489934
ORGANISM: Homo sapiens
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Percent Similarity:
11
Best Local Similarity:
12
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-667-295-15/c
; Sequence 15, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TILLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REPRENCE: 11686-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR PILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 15

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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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NAME/KEY: misc_feature
LOCATION: (1)...(497)
OTHER INFORMATION: Ceres Seq. ID no. 12474809
                                                                                                                                                                         NAME/KEY: misc_feature

; LOCATION: (1)...(475)

; OTHER INFORMATION: Ceres Seq. ID no. 13633589

US-10-667-295-223
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: BASTSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 TCCTCCTAGCCCTCCTTTCAAGA 380
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NAME/KEY: misc feature
LOCATION: (1)...(497)
USTHER INFORMATION: n = A,T,C or US-10-667-295-15
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US-09-925-065A-616675
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Sequence 418469

Dublication No. US2004018104841

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION:

FILE REPERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 09/925,065A

CURRENT FILING DATE: 2001-08-08

FRIOR APPLICATION NUMBER: US 60/243,096

FRIOR PEDICATION NUMBER: US 60/243,096

FRIOR APPLICATION NUMBER: US 60/25,147

PRIOR APPLICATION NUMBER: US 60/25,147

PRIOR APPLICATION NUMBER: US 60/25,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/260,092

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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Publication No. US20050260581A1

GENERAL. INFORMATION:

APPLICANT: FONTANA Maria Rita

APPLICANT: PONTANA Maria Rita

APPLICANT: PAZZA Mariagrazia

APPLICANT: MONACI Blisabeta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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             Conservative:
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CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
                                                                                           Gaps:
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SOFTWARE: SegWin99, version 1.04
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           Percent Similarity:
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US-10-467-657-2511/c
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                                                               Query Match:
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Sequence 616675, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR FILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

SEQ ID NGS: 957086

SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 10827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-00-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOPTWARE: Fastes for Windows Version 4.0
IENGTH: 517
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 TCTGCAGCTGCTGGAATAGCTTCG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 SerAlaAlaAlaGlyIleAlaSer 65
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8.00
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US-09-925-065A-616675
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Best Local Similarity:
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US-09-925-065A-616676
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Pred. No.:
Score:
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DB:
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RESULT 48
US-09-925-065A-151898/c
Sequence 151898, Application US/09925065A
; Bublication No. US20040181048A1
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
    FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-09-08
                                                                                                                                                                                                                                                                                                                               RESULT 47
US-11-021-492-486/C

Sequence 486, Application US/11021492

Sequence 486, Application US/11021492

Sequence 486, Application Woll 1021492

Sequence APPLICANT: Abuin, Alejandro

APPLICANT: Abuin, Alejandro

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Novel Mutated Mammalian Cells and

TITLE OF INVENTION: Novel Mutated Mammalian Cells and

TITLE OF INVENTION: Novel Mutated Mammalian Cells and

TITLE OF INVENTION: Animals

FILE REFERENCE: LEX-0368-USA

CURRENT APPLICATION NUMBER: US/11/021,492

CURRENT FILING DATE: 2001-07-25

NUMBER OF SEQ ID NOS: 698

SEQ ID NO 486

SEQ ID NO 486

LENGTH: 542
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Matches:
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Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature; NAME/KEY: misc_feature; LOCATION: 469, 478, 481, 514, 522, 526; OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                             ) TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2511
                                                                                                   826
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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Pred. No.:
LENGTH: 525
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DB:
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JOURTH APPLICATION NUMBER: US 60/250, 120 PRIOR PLING DATE: 20040181048A1

SEQUENCE 748081, Application US/09925065A

PUBLICACTION NO. US20040181048A1

GENERAL INFORMATION:
APPLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: NUCLECTION PROPRIETS: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER: OF SEQ ID NOS: 957086

SEQ ID NO 748081

LENGTH: 552
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASELSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 151998
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CORGANISM: Homo sapiens
US-09-925-065A-151898
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ORGANISM: Homo gapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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RESULT 53
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                                                                                                                                GENERAL INFUGRATION:
GENERAL INFUGRATION:
JAVICANT:
WANG, DAVIG G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PRICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRILING DATE: 2000-11-30
PRIOR PRILING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR SEQ ID NOS: 957086
SOFTWARE: PRESEQ for Windows Version 4.0
: LENGTH: 559
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PUDLICATION NO. US20040181048A1

GENERAL INFORMATION:

APPLICANT: WANG, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/250,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR AP
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Matches:
Conservative:
Mismatches:
Indels:
                                 Sequence 808255, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-925-065A-808255
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Best Local Similarity:
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US-09-925-065A-808256/c
US-09-925-065A-808255/
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Pred. No.:
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Alignment Scores

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US-09-92-50-08A-808257/C

Sequence 808257, 0820040181048A1

FURICATION NO. US20040181048A1

GENERAL INFORMATION:

APPLICANT: WANG, David G.

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

FRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

FRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

FRIOR PILING DATE: 2000-11-30

FRIOR PILING DATE: 2000-11-30

FRIOR PILING DATE: 2000-11-30

FRIOR PILING DATE: 2000-11-30

FRIOR PILING DATE: 2001-01-16

FRIOR PILING DATE: 2001-01-16
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; Sequence 946604, Application US/09925065A
; Publication No. US20040181048A1
; GRNERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REPERENCE: 108827.135
; CURRENT FILING DATE: 2000-10-08-08
; RICR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR PILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
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Mismatches:
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Length:
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Conservative:
Mismatches:
Indels:
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 808257
LENGTH: 559
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US-09-925-065A-808257
                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-925-065A-808257/c
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Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 946604
LENGTH: 565
                                                                                                                                                                                                    Gaps:
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                                                                                                                                                                                                                                                           490 CTCCCCTCTGCAAGTGCCGCAGCT 513
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                                                                                      TYPE: DNA; ORGANISM: Homo sapiens
US-09-925-065A-946604
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US-09-925-065A-693639
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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US-09-925-065A-693639
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US-09-925-065A-950741
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Pred. No.:
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RESULT 59
US-09-925-065A-53761/c
Sequence 53761, Application US/09925065A
Sequence 53761, Application US/09925065A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION UMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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PRIOR PILING DATE: 2000-10-24
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-01
PRIOR PILING DATE: 2001-01-01
PRIOR PILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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      NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53760
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; ORGANISM: Homo sapiens
US-09-925-065A-53760
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Best Local Similarity:
Query Match:
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LENGTH: 581
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Sequence 854936, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT PELING DATE: 2001-08-08

FRIOR PPLICATION NUMBER: US 60/243,096

FRIOR PPLICATION NUMBER: US 60/252,147

FRIOR PILING DATE: 2000-11-20

FRIOR PPLICATION NUMBER: US 60/250,766

FRIOR PILING DATE: 2001-11-30

FRIOR PILING DATE: 2001-01-16

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/261,766

FRIOR APPLICATION NUMBER: US 60/260,766

FRIOR APPLICATION NUMBER: US 60/280,846

FRIOR SEQ ID NOS: 957086

SEQ ID NO 854936

LENGTH: 576
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US-09-925-065A-854936
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244 GGCTCCCATCTGCCTCTGCTCT 221
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US-09-925-065A-630739/c
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Best Local Similarity:
Query Match:
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LENGTH: 593
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US-09-925-065A-295614/C
i Sequence 295614, Application US/09925065A
; Sequence 295614, Application US/09925065A
; PRUDICATION NO. US20040181048A1
; GENERAL INFORMATION:
    APPLICANT: Wang, David G.
    TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT PLILING DATE: 2000-11-03-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR PRILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/260,092
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR APPLICATION NUMBER: US 60/260,092
; PRIOR PLILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/280,846
; PRIOR APPLICATION NUMBER: US 60/280,846
; PRIOR PLILING DATE: 2001-05-09
; REACHWARE: PESCE FOR WINDOWS VERSION 4.0
; SEQ ID NO 295614
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Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 53762
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Matches:
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ORGANISM: Homo sapiens
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Percent Similarity:
Best Local Similarity:
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Pred. No.:
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GENERAL INVERVATION:
GENERAL INVERVATION:
GENERAL INVERVATION:
TITLE OF INVERVATION: Identification and Mapping of Single
TITLE OF INVERVION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVERVATION: Nucleotide Polymorphisms in the Human Genome
FILE REPRENCE: 108827.135
CURRENT APPLICATION NUMBER: US 60/252,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PELING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2001-01-16
PRIOR SEQ ID NOS: 957086
SOUTHWARE: FASEEGQ for Windows Version 4.0
SEQ ID NO 295459
                                                                                                       TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REPERBNCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/253,096
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
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PRIOR PILING DATE: 2001-01-6
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Matches:
Conservative:
Mismatches:
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; Sequence 630739, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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; Sequence 295459, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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Sequence 301228 sequence 301228 sequence 301228 sequence 301229.

Sequence 301228 sequence 301
                APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 10887.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/25,147
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-7
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-7
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Matches:
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Mismatches:
Indels:
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Matches:
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Mismatches:
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Best Local Similarity:
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US-09-925-065A-301228
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LENGTH: 599
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Pred. No.:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 1)...(595)

; OTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc_feature
LOCATION: 380
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-925-065A-301227
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LENGTH: 595
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Pred. No.:
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US-09-925-065A-774077/C

US-09-925-065A-774077/C

US-09-925-065A-774077/C

Publication No. US20040181048A1

JETUER US INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: UNclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome

FILE REFERENCE: 10827.135

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PLILNG DATE: 2000-10-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-11-30

PRIOR FILING DATE: 2001-01-130

PRIOR PILING DATE: 2001-01-130

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR APPLICATION NUMBER: US 60/289,846
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE NEFERENCE: 108827.135
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US 60/223,147
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR PILING DATE: 2000-11-20
; PRIOR PILING DATE: 2000-11-20
; PRIOR PILING DATE: 2000-11-30
; PRIOR FILING DATE: 2000-11-30
; PRIOR PILING DATE: US 60/251,766
; PRIOR FILING DATE: 2001-01-16
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Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 774077
                                                                                                                                                                                                                    397 AGAGCCCTGCCAAGTTCCTTGGCC 420
                                                                                                                                                                    22 ArgAlaLeuProSerSerLeuAla 29
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; ORGANISM: Homo sapiens
US-09-925-065A-774077
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US-09-925-065A-837176/c
  Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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                                                 Query Match:
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US-11-136-527-8133

Sequence 8133, Application US/11136527

Bublication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Woth

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PLING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOC ID NO 8133

LENGTH: 600
                                                                                                                                                                                                                                                    Sequence 98, Application US/10623155
; Sequence 98, Application US/10623155
; Publication No. US200S0261166A1
; GENERAL INFORMATION:
    APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Penger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS ND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REPREBRUE: 2.1012.455520
; CURRENT FILING DATE: 2003-07-17
; UNMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH 5.00
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                                                                     US-09-989-890-238 (1-212) x US-09-925-065A-301228 (1-599)
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Matches:
Conservative:
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Matches:
Indels:
Gaps:
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                                                                                                                          170 AlaProLeuProValValLeuVal 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | NAME/KEY: misc_feature
| LCCATION: 295, 349, 489, 496, 583
| OTHER INFORMATION: n = A,T,C or G
US-10-623-155-98
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8.00
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                                                      RESULT 67
US-10-623-155-98
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  Query Match:
DB:
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Sequence 893900, Application US/09925065A

Sequence 893900, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-08-08

PRIOR PELING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PILING DATE: 2000-11-16

PRIOR PILING DATE: 2000-10-16

PRIOR PILING DATE: 2000-10-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OP INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-6
PRIOR PILING DATE: 2000-10-16
PRIOR PILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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8.00
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CORGANISM: Homo sapiens
US-09-925-065A-630748
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US-09-925-065A-893900
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-09-925-065A-571840/c

i Sequence 571840, Application US/09925065A

i Sequence 571840, Application US/09925065A

i Publication No. US20040181048A1

i GENERAL INFORMATION:

i APPLICATION NO. Identification and Mapping of Single

i TITLE OF INVENTION: Identification and Mapping of Single

i TITLE OF INVENTION: Identification and Mapping of Single

i TITLE OF INVENTION: Identification and Mapping of Single

i TITLE OF INVENTION: NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-8-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-11-20

PRIOR PPLING DATE: 2000-11-20

PRIOR PPLING DATE: 2000-11-30

PRIOR PPLING DATE: 2000-11-30

PRIOR PPLING DATE: 2001-01-16

PRIOR PPLING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/260,766

PRIOR APPLICATION NUMBER: US 60/260,766

PRIOR PAPLICATION NUMBER: US 60/260,766

NUMBER OF SEC ID NOS: 957086

SOFTWARE FRAEREEQ for Windows Version 4.0

LENGTH: 603
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SSCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 831176
LENGTH: 602
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Sequence 630748, Application US/09925065A

PUblication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.
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US-09-925-065A-837176
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Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                     TYPE: DNA
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR PILING DATE: 2000-10-24
FRIOR PILING DATE: 2000-11-20
FRIOR PILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-46
FRIOR FILING DATE: 2000-11-46
FRIOR FILING DATE: 2001-11-6
FRIOR FILING DATE: 2001-11-6
FRIOR PILING DATE: 2001-01-6
FRIOR FILING DATE: 2001-05-09
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification of Mapping of Single
FILE REFERENCE: 10882-1.135
CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                                      US-09-989-890-238 (1-212) x US-09-925-065A-464419 (1-622)
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                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
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                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-464419
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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LENGTH: 623
SEQ ID NO 464419
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                   LENGTH: 622
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US-09-925-065A-464419, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-00-08

PRIOR PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 957086
                   US-09-989-890-238 (1-212) x US-09-925-065A-893900 (1-611)
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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; ORGANISM: Homo sapiens
US-09-925-065A-749727
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Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence 31084, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/280,846

PRIOR PRIOR DATE: 2001-01-16

PRIOR PRIOR DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PRIOR DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PARISEQ for Windows Version 4.0
SEQ ID NO 686260
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US-09-925-065A-686260
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-925-065A-31084/c
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Pred. No.:
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US-09-925-065A-822330/C

US-09-925-065A-822330/C

Sequence 82230, Application US/09925065A

Publication No. US20040181048A1

GENERAL INPORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 10827.135

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/250,766

PRIOR APPLICATION NUMBER: US 60/269,846

PRIOR APPLICATION NUMBER: US 60/269,846

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
RESULT 79
US-09-925-065A-749727/C
i Sequence 749727/C
i Sequence 749727, Application US/09925065A
i Publication No. US20040181048A1
i GENERAL INFORMATION:
i APPLICANT: Wangy, David G.
i TITLE OF INVENTION: Identification and Mapping of Single
i TITLE OF INVENTION: Identification and Mapping of Single
i TITLE OF INVENTION: NUCLEOCIDE POlymorphisms in the Human Genome
i TITLE OF INVENTION: NUMBER: US/09/925,065A
i CURRENT APPLICATION NUMBER: US 60/243,096
i PRIOR PILING DATE: 2000-10-08-08
i PRIOR PILING DATE: 2000-11-20
i PRIOR PILING DATE: 2000-11-30
i PRIOR PILING DATE: 2001-01-16
i PRIOR APPLICATION NUMBER: US 60/250,092
i PRIOR APPLICATION NUMBER: US 60/261,766
i PRIOR PILING DATE: 2001-01-16
i PRIOR PILING DATE: 2001-01-
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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TYPE: DNA
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US-9-92-065A-883750
is Gequence 883750, Application US/09925065A
is Gequence 883750, Application US/09925065A
is Publication No. US20040181048A1
is GENERAL INFORMATION:
is TITLE OF INVENTION:
is PRIOR APPLICATION NUMBER: US 60/250, 147
is PRIOR APPLICATION NUMBER: US 60/250, 092
is PRIOR PILING DATE: 2000-11-30
is PRIOR PILING DATE: 2000-11-130
is PRIOR PILING DATE: 2000-11-130
is PRIOR PILING DATE: 2000-10-16
is PRIOR PILING DATE: 2001-01-16
is PRIOR FILING DATE: 2001-01-16
is PRIOR FILI
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Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-02-4
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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; ORGANISM: Homo sapiens
US-09-925-065A-883750
                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-925-065A-910175
US-09-925-065A-822330
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FUDILICATION NO. US.20040181048A1

| GENERAL INFORMATION: APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REPERENCE: 108827.135
| CURRENT APPLICATION NUMBER: US/09/925,065A |
| CURRENT PILING DATE: 2001-08-08 |
| PRIOR APPLICATION NUMBER: US 60/243,096 |
| PRIOR PILING DATE: 2000-11-20 |
| PRIOR PILING DATE: 2000-11-20 |
| PRIOR FILING DATE: 2000-11-30 |
| PRIOR FILING DATE: 2001-01-16 |
| PRIOR FILING DATE: 2001-01-16 |
| PRIOR FILING DATE: 2001-01-16 |
| PRIOR FILING DATE: 2001-01-6 |
| PRIOR FILING DATE: 2001-05-09 |
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 910175
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CORGANISM: Homo sapiens
US-09-925-065A-709912
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US-09-925-065A-910175
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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Pred. No.:
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RESULT BESULT BY SEASON OF SEASON OF SEQUENCE 4578, Application US/09925065A

Sequence 4578, Application US/09925065A

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REPRENCE: 108827.135

CURRENT FILING DATE: 2001-08-08

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 95-006

SEQ ID NOS: 95-006

SEQ ID NO 45-78

LENGTH A. 64-4
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108927.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
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     Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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                                                                                                                                                                                                           24 LeuProSerSerLeuAlaLeuLeu 31
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ORGANISM: Homo sapiens
                             Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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DB:
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Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Number: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER: PSESQ ID NOS: 957086

SOFTWARE: PSESEQ for Windows Version 4.0

SEQ ID NO 4577

LENGTH: 644
                                                                                            APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR PELICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-05-09
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                       Sequence 441386, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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US-09-925-065A-441386
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US-09-925-065A-4577
US-09-925-065A-441386/c
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Best Local Similarity:
Query Match:
DB:
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US-09-925-065A-4577/c
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LENGTH: 662
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Pred. No.:
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Pred. No.:
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Sequence 91, Application US/11103957
Fublication No. US20050281847A1
Fublication No. US20050281847A1
GENERAL INFORMATION:
APPLICANT: Berthet, Francois-Xavier Jacques
APPLICANT: Lobet, Yves
APPLICANT: Verlant, Vincent Georges Christian Louis
TITLE OF INVENTION: Vaccine Composition
FILE REFERENCE: B45261
CURRENT APPLICATION NUMBER: US/11/103,957
CURRENT FILING DATE: 2005-04-12
FRIOR APPLICATION NUMBER: PCT/EP02/01356
FRIOR APPLICATION NUMBER: CT/EP02/01356
FRIOR APPLICATION NUMBER: G0 0103169.9
FRIOR FILING DATE: 2001-02-08
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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Matches:
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4579
LENGTH: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
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(US-11-077-619-41/C
US-11-077-619-41/C
Sequence 41, Application US/11077619
Publication No. US20060040279A1
GENERAL INFORMATION
APPLICANT: Feesche, Oserg
APPLICANT: Maurer, Karl-Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-11-103-957-91
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3.8%
                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-4579
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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US-11-103-957-91/c
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Pred. No.:
Score:
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Pred. No.:
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US-20-214-780/C

Sequence 780, Application US/10821234

Publication No. US2050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Abat, Ivan
APPLICANT: Abat, Ivan
APPLICANT: And Y. Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFRENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR APPLICATION NUMBER: US 60/462,047

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: PL-SEQ_Genes Version 1.0

LENGTH: 855
APPLICANT: Schweder, Thomas
APPLICANT: Becker, Michael
APPLICANT: Hecker, Michael
APPLICANT: Udergen, Britta
APPLICANT: Udergen, Britta
APPLICANT: Voigt, Britta
APPLICANT: Voigt, Bright
TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
FILE REFERENCE: HENK-0122 / H5592
CURRENT APPLICATION NUMBER: US/11/077,619
CURRENT FILING DATE: 2005-03-11
PRIOR FILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-11
NUMBER: OF SEQ ID NOS: 130
SOFTWARE: Patentin version 3.3
SEQ ID NO 41
LENGTH: 829
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Escherichia coli
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LOCATION: (1)..(829)
OTHER INFORMATION: ibpB
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US-10-821-234-780
                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (201)..(629)
US-11-077-619-41
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Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence 63837, Application US/09925065A
; Bublication No. US20040181048A1
; Germeral information No. US20040181048A1
; Germeral information No. US20040181048A1
; GERERAL INFORMATION: Identification and Mapping of Single
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR PILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR PILING DATE: 2001-01-130
; PRIOR PILING DATE: 2001-01-16
; PRIOR PILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR PILING DATE: 2001-01-16
; PRIOR PILING DATE: 2001-01-16
; PRIOR PILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/289,846
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 GCCTGCCCAGTTCTCTGGCCCTA 233
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                                                                                                                                           FEATURE:

NAME/KEY: misc feature

LOCATION: (492)...(512)

OTHER INFORMATION: n is a, c,
US-11-128-049-61
SOFTWARE: Patentin version 3.3
SEQ ID NO 61
LENGTH: 1002
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                                                                                      TYPE: DNA ORGANISM: Cricetulus griseus
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-925-065A-63838/c
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US-11-128-049-61

Squence 61, Application US/11128049

Publication No. US20060010513A1

GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Mounts, William M.
APPLICANT: Hann, Louane B.
APPLICANT: Brown, Rugene E.
APPLICANT: Brown, Rugene L.
APPLICANT: Brown, Rugene L.
APPLICANT: APPLICANT: Willer, Christopher P.
TITLE OF INVENTION: OLICONUCLECTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR TITLE OF INVENTION: MAKING AND USING SAME
FILLE REPERENCE: 01997.027700

CURRENT APPLICATION NUMBER: US/11/128,049

CURRENT FILLING DATE: 2005-05-11
                                                                                                                                                                                                          Sequence 61, Application US/11128061

Publication No. US2006000395841

GENERAL IRPORMATION:

APPLICANT: Melville, Mark W.

APPLICANT: Mounts, William M.

APPLICANT: Hann, Louene E.

APPLICANT: Hann, Louene E.

APPLICANT: Leonard, Mark W.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDE ARRAYS

TITLE OF INVENTION: TO MONITOR GENE EXPRESSION

CURRENT PILING DATE: 2005-05-11

CURRENT PILING DATE: 2005-05-11

PRIOR FILING DATE: 2004-05-11

NUMBER OF SEQ ID NOS: 7285

SEQ ID NO 61

ENGTHA I 1002

LENGTH 1002
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Matches:
Conservative:
Mismatches:
Indels:
US-09-989-890-238 (1-212) x US-10-821-234-780 (1-855)
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PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
i LOCATION: (492)...(512)
i OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-61
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Query Match:
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Pred. No.:
                                                                                                                                                                      RESULT 91
US-11-128-061-61
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RESULT 97
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PUBLICATION NO. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

TITLE REPRENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-11-36

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR SEQ ID NOS: 957086

SOFTWARE: FASELEQ for Windows Version 4.0

LENGTH: 1038
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63838
LENGTH: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-989-890-238 (1-212) x US-09-925-065A-63838 (1-1038)
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Matches:
Conservative:
Mismatches:
Indels:
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CORGANISM: Homo sapiens
US-09-925-065A-63838
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US-09-925-065A-63839/c
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APPLICANT: FERNANDEZ, EMILIO O.
APPLICANT: FERNANDEZ, EMILIO O.
APPLICANT: GOCABAS, ARIF
APPLICANT: GOCABAS, ARIF
APPLICANT: CROSHAS, ARIF
APPLICANT: CROSHS, JAVIER A.
TITLE OF INVENTION: IDENTIPICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
TITLE OF INVENTION: UABILITY
FILE OF INVENTION: UABILITY
FILE OF INVENTION: UMBER: US/11/091,883
CURRENT FILING DATE: 2005-03-29
RICH REPERRORE: 5394208
CURRENT FILING DATE: 2006-03-29
RICH REPERRORES FOR THE APPLICATION NUMBER: 60/556,875
PRIOR FILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 513
SEQ ID NO 130
LENGTH: 1044
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JAPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Incleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/225,147
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01
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                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 130, Application US/11091883; Publication No. US20060024693A1; GENERAL INFORMATION: APPLICANT: CIBELLI, JOSE
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PLILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASESEQ FOR Windows Version 4.0
                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-578
                                                                                                                                                                       LENGTH: 1056
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
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US-09-925-065A-576
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; ORGANISM: Homo sapiens
US-09-925-065A-577
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RESULT 100
US-09-925-065A-579
Sequence 579, Application US/09925065A
Sequence 579, Application US/09925065A
Sequence 579, Application No. US20040181048A1
GENERAL INFORMATION:
TAPLICANT: Wang David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Molectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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                Length:
Matches:
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Matches:
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CURRENT FILING DATE: 2001-08-08
PRIOR PELING DATE: 2001-024
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
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PRIOR PILING DATE: 2001-01-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 579
LENGTH: 1056
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; ORGANISM: Homo sapiens
US-09-925-065A-579
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Query Match:
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Search completed: March 17, 2006, 07:00:40 Job time : 1316 secs